

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2004, 15:29:03 ; Search time 162 Seconds
(without alignments)
460.591 Million cell updates/sec

Title: US-10-019-065A-1
Perfect score: 1231
Sequence: 1 QVHGFRQSAWRACSVTCG.....SCGGARQRTGCSDPVPOY 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1231	100.0	208	5 AAB47770	Aab47770 Human thr
2	1231	100.0	707	6 ABU69134	Abu69134 Human NOV
3	1231	100.0	707	8 ADH72102	Adh72102 Human pro
4	1231	100.0	707	8 ADO08271	Ado08271 Human NOV
5	1231	100.0	1336	5 AAB47771	Aab47771 Human thr
6	1231	100.0	1708	7 ADG39841	Adg39841 Protein s
7	1231	100.0	1708	7 ADG39840	Adg39840 Protein s
8	1231	100.0	1902	6 ABU12084	Abu12084 Human NOV
9	1231	100.0	1902	6 ADH72108	Adh72108 Human pro
10	1231	100.0	5635	5 ABP60991	Abp60991 Novel hum
11	1231	100.0	5636	7 ADJ70089	Adj70089 Human hea
12	1231	100.0	5636	7 ADJ8137	Adj8137 Human hem
13	1231	100.0	5636	8 ADK60205	Adk60205 Angiogene
14	1231	100.0	5636	8 ADK60506	Adk60506 Angiogene
15	1231	100.0	5636	8 ADK60506	Adk60506 Angiogene
16	1230	99.9	1708	7 ADG39844	Adg39844 Protein s
17	1230	99.9	2572	6 ABU12083	Abu12083 Human NOV
18	1230	99.9	2673	8 ADK60225	Adk60225 Angiogene
19	1230	99.9	2673	8 ADK60526	Adk60526 Angiogene
20	1230	99.9	2673	8 ADK60526	Adk60526 Angiogene
21	1230	99.9	3645	7 ADH73149	Adh73149 Angiogene
22	1230	99.9	4495	6 ADH73136	Adh73136 Human hem
23	1230	99.9	4495	8 ABU69135	Abu69135 Human NOV
24	1230	99.9	4495	8 ADH72106	Adh72106 Human pro
25	1221	99.2	712	8 ADO08273	Ado08273 Human NOV
					Adh72104 Human pro

ALIGNMENTS

RESULT 1
AAB47770
ID AAB47770 standard; peptide; 208 AA.

XX AC AAB47770;
XX DT 04-MAR-2002 (first entry)
XX DE Human thrombospondin protein, BTL.012, fragment 654-861.
XX KW Human; thrombospondin; BTL.012; thrombospondin repeat domain; modulation;
XX KW angiogenesis; cancer; metastasis; diabetic retinopathy;
XX KW macular degeneration; cardiovascular disease; wound.
XX OS Homo sapiens.
XX PN WO200174852-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US010222.
XX PR 31-MAR-2000; 2000US-0266300P.
XX (FARB) BAYER CORP.
XX PI Chen J, Chen D, Zolotarev A, Davies CJ, Wetzel GD;
XX PI Dubois-Stringfellow NA;
XX WPI; 2002-066297/09.

Novel protein designated BTL.012 has a thrombospondin repeat and inhibits angiogenesis, and is useful to treat cancer, diabetic retinopathy, macular degeneration, cardiovascular disease and wounds.
Claim 2; Page 35; 54pp; English.
This sequence represents a fragment of the human thrombospondin protein, BTL.012. This peptide, comprising a thrombospondin repeat domain, may be used to modulate angiogenesis at a site. This BTL.012 fragment may be used for diagnosing, preventing or treating a medical condition, particularly cancer, metastasis, diabetic retinopathy, macular degeneration, cardiovascular disease or a wound

Sequence 208 AA;

Query Match 100.0%; Score 1231; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 9.9e-89;

Matches	208;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	QVHGFSQSAWRACSVTCGKGIQKRSRLCNQPLPANGGKPCQGSLEMRNCQNKPCPYD	60						
Db	1	QVHGFSQSAWRACSVTCGKGIQKRSRLCNQPLPANGGKPCQGSLEMRNCQNKPCPYD	60						
QY	61	GSWSESLWEECTRCGRGNQTRTRTCNNPVSQHGGRPCGNAVEIIMCNIRPCPVHGAW	120						
Db	61	GSWSESLWEECTRCGRGNQTRTRTCNNPVSQHGGRPCGNAVEIIMCNIRPCPVHGAW	120						
QY	121	SAWQPMGTCSGCGTQTRARLCNNPPATGGSYCDGAETQMOVCNERNCPHGWATW	180						
Db	121	SAWQPMGTCSGCGTQTRARLCNNPPATGGSYCDGAETQMOVCNERNCPHGWATW	180						
QY	181	ASWSACSVSCGGARQTRGCSDPVPOY	208						
Db	181	ASWSACSVSCGGARQTRGCSDPVPOY	208						
RESULT 2									
ABU69134									
ID	ABU69134	standard; protein; 707 AA.							
XX	AC	ABU69134;							
XX	DT	02-JUN-2003 (first entry)							
XX	DE	Human NOVX polypeptide #9.							
XX	KW	Human; NOVX; metabolic disorder; diabetes; infectious disease; obesity;							
XX	KW	anorexia; cancer; cardiovascular disorder; asthma; neurogenesis;							
XX	KW	neurodegenerative disorder; epilepsy; immune disorder; osteoarthritis;							
XX	KW	haematopoietic disorder; inflammatory skin disorder; dyslipidemia;							
XX	KW	haematopoiesis; wound healing; angiogenesis; bacterial infection;							
XX	KW	viral infection; fungal infection; helminthic infection; atherosclerosis;							
XX	KW	protozoal infection; hypertension.							
OS		Homo sapiens.							
XX	PN	WO200290504-A2.							
XX	PD	14-NOV-2002							
XX	PF	02-MAY-2002; 2002WO-US014342.							
XX	PR	03-MAY-2001; 2001US-0288395P.							
XX	PR	04-MAY-2001; 2001US-0288900P.							
XX	PR	07-MAY-2001; 2001US-0289087P.							
XX	PR	14-MAY-2001; 2001US-0290753P.							
XX	PR	15-MAY-2001; 2001US-0291189P.							
XX	PR	16-MAY-2001; 2001US-0291243P.							
XX	PR	18-MAY-2001; 2001US-0292001P.							
XX	PR	21-MAY-2001; 2001US-0292374P.							
XX	PR	22-MAY-2001; 2001US-0292587P.							
XX	PR	23-MAY-2001; 2001US-0293107P.							
XX	PR	29-MAY-2001; 2001US-0294110P.							
XX	PR	30-MAY-2001; 2001US-0294434P.							
XX	PR	31-MAY-2001; 2001US-0294827P.							
XX	PR	18-JUN-2001; 2001US-0298988P.							
XX	PR	31-JUL-2001; 2001US-0308901P.							
XX	PR	17-AUG-2001; 2001US-0313388P.							
XX	PR	21-AUG-2001; 2001US-0313851P.							
XX	PR	21-AUG-2001; 2001US-0313937P.							
XX	PR	17-SEP-2001; 2001US-0322701P.							
XX	PR	17-SEP-2001; 2001US-0322802P.							
XX	PR	25-SEP-2001; 2001US-0324757P.							
XX	PR	27-SEP-2001; 2001US-0325314P.							
XX	PR	27-SEP-2001; 2001US-0325682P.							
XX	PR	21-NOV-2001; 2001US-0332129P.							
XX	PR	03-DEC-2001; 2001US-0336882P.							
XX	PR	14-DEC-2001; 2001US-0340305P.							
XX	PR	01-MAY-2002; 2002US-00138588.							

PA	XX	(CURA-) CURAGEN CORP.
PI	XX	Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Casman SJ;
PI	XX	Chapoval A, Edinger S, Gerlach V, Gorman L, Gunther E, Guo X;
PI	XX	Kekuda R, Lepley DM, Li L, Liu X, Malvankar UM, Miller CE;
PI	XX	Milliet I, Padigaru M, Patturajan M, Pena CE, Rieger DK, Shenoy SG;
PI	XX	Shinkets RA, Spytek KA, Taupier RJ, Vernet CAM, Voss EZ;
PI	XX	Zerhusen BD;
XX	XX	WPI: 2003-103512/09.
DR	XX	N-PSDB; ACA10119.
PT	XX	New isolated NOVX polypeptides and polynucleotides, useful for
PT	XX	preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT	XX	osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT	XX	asthma, or infections.
XX	XX	Claim 2; Page 101; 340pp; English.
XX	XX	The invention relates to human NOVX polypeptides and the polynucleotides
CC	XX	encoding them. The polypeptides, polynucleotides and antibodies that bind
CC	XX	immunosepecifically to the polypeptides are useful in the manufacture of a
CC	XX	medicament for treating a syndrome associated with a human disease,
CC	XX	preferably a NOVX-associated disorder. The sequences are useful for
CC	XX	treating, preventing or diagnosing diseases such as metabolic disorders,
CC	XX	diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC	XX	helminthic, and protozoal), anorexia, cancer, cardiovascular disorders
CC	XX	(e.g. hypertension, atherosclerosis), neurodegenerative disorders (e.g.
CC	XX	Alzheimer's disease, Parkinson's disease), epilepsy, immune disorders,
CC	XX	osteoarthritis, haematopoietic disorders, inflammatory skin disorders,
CC	XX	asthma and various dyslipidemias. The nucleic acids and polypeptides may
CC	XX	also be used as targets for the identification of small molecules that
CC	XX	modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC	XX	proliferation, haematopoiesis, wound healing and angiogenesis, and in the
CC	XX	generation of antibodies that bind immunosepecifically to NOVX substances
CC	XX	for use in therapeutic or diagnostic methods. The nucleic acids are
CC	XX	further used as hybridisation probes, and in chromosome mapping, tissue
CC	XX	typing, preventive medicine and pharmacogenomics. Sequences ABU69126-
CC	XX	ABU69171 represent human NOVX polypeptides of the invention
XX	XX	Sequence 707 AA;
SQ	XX	Query Match 100.0%; Score 1231; DB 6; Length 707;
		Best Local Similarity 100.0%; Pred. No. 3.3e-88;
		Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	QVHGFSQSAWRACSVTCGKGIQKRSRLCNQPLPANGGKPCQGSLEMRNCQNKPCPYD 60
Db	471	QVHGFSQSAWRACSVTCGKGIQKRSRLCNQPLPANGGKPCQGSLEMRNCQNKPCPYD 530
QY	61	GSWSESLWEECTRCGRGNQTRTRTCNNPVSQHGGRPCGNAVEIIMCNIRPCPVHGAW 120
Db	531	GSWSESLWEECTRCGRGNQTRTRTCNNPVSQHGGRPCGNAVEIIMCNIRPCPVHGAW 590
QY	121	SAWQPMGTCSGCGTQTRARLCNNPPATGGSYCDGAETQMOVCNERNCPHGWATW 180
Db	591	SAWQPMGTCSGCGTQTRARLCNNPPATGGSYCDGAETQMOVCNERNCPHGWATW 650
QY	181	ASWSACSVSCGGARQTRGCSDPVPOY 208
Db	651	ASWSACSVSCGGARQTRGCSDPVPOY 678
RESULT 3		
ADH72102		
ID	ADH72102	standard; protein; 707 AA.
XX	AC	ADH72102;
XX	DT	25-MAR-2004 (first entry)
XX	DE	Human protein of the invention NOV43a SEQ ID NO:998.

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
 KW anorectic; anti-diabetic; antidiabetic; antidiabetic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.

OS Homo sapiens.

PN WO2003102155-A2.

XX 11-DEC-2003.

PF 03-JUN-2003; 2003WO-US017430.

XX 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 06-JUN-2002; 2002US-0386047P.

PR 07-JUN-2002; 2002US-0386376P.

PR 08-JUN-2002; 2002US-0386453P.

PR 09-JUN-2002; 2002US-0386864P.

PR 10-JUN-2002; 2002US-0387016P.

PR 11-JUN-2002; 2002US-0386796P.

PR 12-JUN-2002; 2002US-0386916P.

PR 13-JUN-2002; 2002US-0386931P.

PR 14-JUN-2002; 2002US-0386942P.

PR 15-JUN-2002; 2002US-0386971P.

PR 16-JUN-2002; 2002US-0387462P.

PR 17-JUN-2002; 2002US-0296960P.

PR 18-JUN-2002; 2002US-0387400P.

PR 19-JUN-2002; 2002US-0387535P.

PR 20-JUN-2002; 2002US-0387610P.

PR 21-JUN-2002; 2002US-0387625P.

PR 22-JUN-2002; 2002US-0387634P.

PR 23-JUN-2002; 2002US-0387658P.

PR 24-JUN-2002; 2002US-0387696P.

PR 25-JUN-2002; 2002US-0387702P.

PR 26-JUN-2002; 2002US-0387836P.

PR 27-JUN-2002; 2002US-0387859P.

PR 28-JUN-2002; 2002US-0387933P.

PR 29-JUN-2002; 2002US-0387934P.

PR 30-JUN-2002; 2002US-0387960P.

PR 31-JUN-2002; 2002US-0388022P.

PR 32-JUN-2002; 2002US-0388096P.

PR 33-JUN-2002; 2002US-0389123P.

PR 34-JUN-2002; 2002US-0389180P.

PR 35-JUN-2002; 2002US-0389144P.

PR 36-JUN-2002; 2002US-0389146P.

PR 37-JUN-2002; 2002US-0389729P.

PR 27-AUG-2002; 2002US-0406240P.

PR 28-SEP-2002; 2002US-0410084P.

PR 29-SEP-2002; 2002US-0412528P.

PR 30-SEP-2002; 2002US-0412731P.

PR 31-SEP-2002; 2002US-0414801P.

PR 32-SEP-2002; 2002US-0414839P.

PR 33-SEP-2002; 2002US-0414840P.

PR 34-SEP-2002; 2002US-0414954P.

PR 35-SEP-2002; 2002US-0417186P.

PR 36-SEP-2002; 2002US-0417406P.

PR 37-SEP-2002; 2002US-0420639P.

PR 38-SEP-2002; 2002US-0421156P.

PR 39-SEP-2002; 2002US-0422690P.

PR 40-SEP-2002; 2002US-0423130P.

PR 41-SEP-2002; 2002US-0423798P.

PR 42-SEP-2002; 2002US-0423798P.

PR 43-SEP-2002; 2002US-0425453P.

XX (CURA-) CURAGEN CORP.

XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;

XX Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;

XX Eitenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;

XX Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;

XX MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;

XX Padigaru M, Patturajan M, Pena CEA, Peyman ZA, Raha D, Rastelli L;

XX Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;

XX Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;

XX Zhong H;

XX WPI; 2004-081935/08.

XX N-PSDB; ADH72101.

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or

XX treating NOVX-associated disorders, e.g. cancer, diabetes, infection or

XX obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 43; SEQ ID NO 998; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A

XX polypeptide of the invention has cytostatic, immunomodulator,

XX neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and

XX antiproliferative activity, and may have a use in gene therapy, and as a

XX vaccine. The polypeptides are encoded by NOVX polynucleotides comprising

XX any of the 303 fully defined nucleotide sequences given in the

XX specification. The polypeptide is useful in the manufacture of a

XX medicament for treating a syndrome associated with a human disease. The

XX polypeptide, polynucleotide and antibody are useful in diagnosing,

XX treating or preventing NOVX-associated disorders, e.g. cancer, diabetes, infection or

XX obesity, and in chromosome mapping, tissue typing or pharmacogenomics. The present sequence

XX represents a NOVX polypeptide of the invention.

XX Query Match 100.0%; Score 1231; DB 8; Length 707;

XX Best Local Similarity 100.0%; Pred. No. 3.3e-88;

XX Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 QVHGGFSQWAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQSDLEMRNCKNPKCPVD 60

XX 471 QVHGGFSQWAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQSDLEMRNCKNPKCPVD 530

XX 61 GSWSEWSLWEECTRCGRGNQTRTTCNNPSVQHGGRCEGNVAIIICNTRPCPVHGAW 120

XX 531 GSWSEWSLWEECTRCGRGNQTRTTCNNPSVQHGGRCEGNVAIIICNTRPCPVHGAW 590

XX 121 SAWQPMGTCSGCGKGTQTRARLNNPPPAFGSGYCDGAETQMVQCNERNCPHKGKATW 180

XX 591 SAWQPMGTCSGCGKGTQTRARLNNPPPAFGSGYCDGAETQMVQCNERNCPHKGKATW 650

QY 181 ASWSACSVSCGGARQRTGCSDFVPOY 208
 Db 651 ASWSACSVSCGGARQRTGCSDFVPOY 678

RESULT 4
 ADO08271
 ID ADO08271 standard; protein; 707 AA.
 AC ADO08271;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human NOVX polypeptide #9.
 XX
 KW Human; NOVX; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
 KW obesity; cancer; diabetes; haemophilia; graft-versus-host disease; AIDS;
 KW asthma; Crohn's disease; multiple sclerosis; infection; anorexia;
 KW cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; haematopoietic disorder;
 KW wasting disorder.
 XX
 OS Homo sapiens.
 XX
 PN US2004018594-A1.
 XX
 PD 29-JAN-2004.
 XX
 PF 01-MAY-2002; 2002US-00138588.
 XX
 PR 03-MAY-2001; 2001US-0288395P.
 PR 04-MAY-2001; 2001US-0288900P.
 PR 07-MAY-2001; 2001US-0289087P.
 PR 14-MAY-2001; 2001US-0290753P.
 PR 15-MAY-2001; 2001US-0291189P.
 PR 16-MAY-2001; 2001US-0291243P.
 PR 18-MAY-2001; 2001US-0292001P.
 PR 21-MAY-2001; 2001US-0292374P.
 PR 22-MAY-2001; 2001US-0292587P.
 PR 23-MAY-2001; 2001US-0293107P.
 PR 29-MAY-2001; 2001US-0294110P.
 PR 30-MAY-2001; 2001US-0294434P.
 PR 31-MAY-2001; 2001US-0294827P.
 PR 31-JUL-2001; 2001US-030901P.
 PR 17-AUG-2001; 2001US-031388P.
 PR 21-AUG-2001; 2001US-0313851P.
 PR 21-AUG-2001; 2001US-0313937P.
 PR 17-SEP-2001; 2001US-0322701P.
 PR 17-SEP-2001; 2001US-0322802P.
 PR 25-SEP-2001; 2001US-0324757P.
 PR 27-SEP-2001; 2001US-0325314P.
 PR 27-SEP-2001; 2001US-0325682P.
 PR 21-NOV-2001; 2001US-0332129P.
 PR 03-DEC-2001; 2001US-0336882P.
 PR 14-DEC-2001; 2001US-0340305P.

(ALSO/) ALSBROOK J P.
 (ANDE/) ANDERSON D W.
 PA (BOLD/) BOLDOG F L.
 PA (BURG/) BURGESS C E.
 PA (CASM/) CASMAN S J.
 PA (CHAP/) CHAPOVAL A.
 PA (EDIN/) EDINGER S R.
 PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 PA (GUNT/) GUNTHER E.
 PA (GUOX/) GUO X S.
 PA (KEKU/) KEKUDA R.
 PA (LEPL/) LEFLEY D M.
 PA (LILL/) LI L.
 PA (LIUX/) LIU X.
 PA (MALY/) MALYANKAR U M.
 PA (MILL/) MILLER C E.

PA (MILL/) MILLET I.
 PA (PADI/) PADIGARU M.
 PA (PATT/) PATTURAJAN M.
 PA (PENA/) PENA C E A.
 PA (RIEG/) RIEGER D K.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (SPIT/) SPYTEK K A.
 PA (TAUP/) TAUPIER R J.
 PA (VERN/) VERNET C A M.
 PA (VOSS/) VOSS E Z.
 PA (ZERH/) ZERHUSEN B D.
 XX
 PI Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Casman SJ;
 PI Chapoval A, Edinger SR, Gerlach V, Gorman L, Gunther E, Guo XS;
 PI Kekuda R, Lepley DM, Li L, Liu X, Malvankar UM, Miller CE;
 PI Millet I, Padigar M, Patturajan M, Pena CEA, Rieger DK, Shenoy SG;
 PI Shimkets RA, Sytek KA, Taupier RJ, Vernet CM, Voss EZ;
 PI Zerhusen BD;
 XX
 DR WPI; 2004-122037/12.
 DR N-FSDB; ADO08270.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes,
 PT atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing
 PT or pharmacogenomics.
 XX
 PS Claim 2; SEQ ID NO 18; 219pp; English.
 XX
 CC The invention relates to human NOVX polypeptides and the polynucleotides
 CC encoding them. The polypeptides, polynucleotides and antibodies that bind
 CC immunospecifically to the polypeptides are useful in diagnosing, treating
 CC or preventing NOVX-associated disorders such as cardiomyopathy,
 CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,
 CC haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,
 CC multiple sclerosis, infections, anorexia, cancer-associated cachexia,
 CC neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's
 CC disease), haematopoietic disorders and wasting disorders. The
 CC polynucleotides are also used as hybridisation probes, in chromosome
 CC mapping and in tissue typing. The polypeptides are also useful as
 CC vaccines. This sequence represents a human NOVX polypeptide of the
 CC invention.
 XX
 SQ Sequence 707 AA;
 Query Match 100.0%; Score 1231; DB 8; Length 707;
 Best Local Similarity 100.0%; Pred. No. 3.3e-88;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVHGGSFQSWASACSVTCGKGIQKESRLCNQPLPANGKPCQGSDEMRNCKNKPVD 60
 Db 471 QVHGGSFQSWASACSVTCGKGIQKESRLCNQPLPANGKPCQGSDEMRNCKNKPVD 530
 QY 61 GSWSESLWEECTRCGRGNQTRTRTCNNPVSQHGRCPCGNVAVIIMCNIIRPCPVHGA 120
 Db 531 GSWSESLWEECTRCGRGNQTRTRTCNNPVSQHGRCPCGNVAVIIMCNIIRPCPVHGA 590
 QY 121 SAWQPMGTCSGCGKTQTRARLCNNPPAPFGSGYCDGAETQMOVCNERNCPHGWATW 180
 Db 591 SAWQPMGTCSGCGKTQTRARLCNNPPAPFGSGYCDGAETQMOVCNERNCPHGWATW 650
 QY 181 ASWSACSVSCGGARQRTGCSDFVPOY 208
 Db 651 ASWSACSVSCGGARQRTGCSDFVPOY 678

RESULT 5
 AAB47771
 ID AAB47771 standard; protein; 1336 AA.
 XX
 AC AAB47771;
 XX

DT XX 04-MAR-2002 (first entry)
DE XX Human thrombospondin protein, BTL.012.
XX
KW Human; thrombospondin; BTL.012; thrombospondin repeat domain; modulation;
KW angiogenesis; cancer; metastasis; diabetic retinopathy;
KW macular degeneration; cardiovascular disease; wound.
XX
OS Homo sapiens.
XX
FH Key
FH 657..711 Location/Qualifiers
FT Domain
FT /label= thrombospondin domain type I repeat - a
FT 714..768
FT /label= thrombospondin domain type I repeat - b
FT 771..825
FT /label= thrombospondin domain type I repeat - c
FT 828..882
FT /label= thrombospondin domain type I repeat - d
FT 885..939
FT /label= thrombospondin domain type I repeat - e
FT 942..996
FT /label= thrombospondin domain type I repeat - f
FT Misc-difference 1325
FT /label= Encoded by GAA
XX
XX WO200174852-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US010222.
XX
XX 31-MAR-2000; 2000US-0266300P.
XX
XX (FARB) BAYER CORP.
XX
XX Chen J., Chen D., Zolotorev A., Davies CJ, Wetzel GD;
XX Dubois-Stringfellow NA;
XX
XX WPI; 2002-066297/09.
XX N-PSDB; AAI72024.
XX
XX Novel protein designated BTL.012 has a thrombospondin repeat and inhibits
XX angiogenesis, and is useful to treat cancer, diabetic retinopathy,
XX macular degeneration, cardiovascular disease and wounds.
XX
XX Claim 21; Page 49-53; 54pp; English.
XX
XX This sequence represents a human thrombospondin protein, BTL.012. A
XX fragment of this protein, comprising a thrombospondin repeat domain, may
XX be used to modulate angiogenesis at a site. The BTL.012 fragment may be
XX used for diagnosing, preventing or treating a medical condition,
XX particularly cancer, metastasis, diabetic retinopathy, macular
XX degeneration, cardiovascular disease or a wound
XX
XX Sequence 1336 AA;
XX
XX Query Match 100.0%; Score 1231; DB 5; Length 1336;
XX Best Local Similarity 100.0%; Pred. No. 6.3e-88;
XX Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 QVHGFGSQAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDELNRNCKNPKCPVD 60
XX 654 QVHGFGSQAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDELNRNCKNPKCPVD 713
XX
XX 61 GSKSEWSLWEETRSCGNGNTRTCTNNPVSQHGGRPCGNAVEIIMCNIRPCPVHGAW 120
XX 714 GSKSEWSLWEETRSCGNGNTRTCTNNPVSQHGGRPCGNAVEIIMCNIRPCPVHGAW 773
XX
XX 121 SAWQPMGTCSGCGKGTQTFARLCNNPPAFGGSYCDGAETQMQVCNERNCPFHGKWATW 180
XX 774 SAWQPMGTCSGCGKGTQTFARLCNNPPAFGGSYCDGAETQMQVCNERNCPFHGKWATW 833
XX Db

QY 181 ASWSACSUSCGGARQRTGCGSDPVPQY 208
Db 834 ASWSACSUSCGGARQRTGCGSDPVPQY 861

RESULT 6
ADG39841
ID ADG39841 standard; protein; 1708 AA.
XX
XX AC ADG39841;
XX
XX 26-FEB-2004 (first entry)
XX
XX Protein similar to human NOV9 #2.
XX
XX Human; NOVX; cardiomyopathy; atherosclerosis; hypertension;
KW congenital heart defect; pulmonary stenosis; scleroderma; obesity;
KW metabolic disturbance; obesity; transplantation; adrenoleukodystrophy;
KW congenital adrenal hyperplasia; prostate cancer; diabetes;
KW metabolic disorder; neoplasm; adenocarcinoma; fertility; haemophilia;
KW graft versus host disease; AIDS; bronchial asthma; Crohn's disease;
KW multiple sclerosis; infectious disease; anorexia;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia;
KW wasting disorder.
XX
XX OS Homo sapiens.
XX
XX PN US2003203843-A1.
XX
XX PD 30-OCT-2003.
XX
XX 11-APR-2002; 2002US-00120801.
XX
XX 20-APR-2001; 2001US-0285609P.
XX 23-APR-2001; 2001US-0285748P.
XX 24-APR-2001; 2001US-0286068P.
XX 25-APR-2001; 2001US-0286292P.
XX 03-MAY-2001; 2001US-0288334P.
XX 16-MAY-2001; 2001US-0291241P.
XX 14-SEP-2001; 2001US-0322284P.
XX
XX (PENA/) PENA C E A.
XX (GUOX/) GUO X.
XX (SHIM/) SHIMKETS R A.
XX (PADI/) PADIGARU M.
XX (KEKU/) KEKUDA R.
XX (SPYT/) SPYTEK K A.
XX (MEHR/) MEHRABAN F.
XX (TOPP/) TOPPER J N.
XX (MALY/) MALYANKAR U M.
XX (WASS/) WASSERMAN S M.
XX (EDIN/) EDINGER S R.
XX (SMIT/) SMITHSON G.
XX (GUNT/) GUNTHER E.
XX (KOMU/) KOMUVES L.
XX
XX Pena CEA, Guo X, Shimkets RA, Padigaru M, Kekuda R, Spytek KA;
XX Mehraban F, Topper JN, Malyankar UM, Wasserman SM, Edinger SR;
XX Smithson G, Gunther E, Komuves L;
XX
XX WPI; 2003-900671/82.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing or
XX treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma,
XX obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or
XX multiple sclerosis.
XX
XX Disclosure; SEQ ID NO 73; 215pp; English.
XX
XX The invention relates to a new isolated polypeptide comprising an amino
XX acid sequence selected from 17 fully defined human NOVX sequences (even
XX SEQ ID NOS between ADG39770 and ADG39802), a mature form of the NOVX

CC amino acid or a variant of NOVX, where one or more amino acid residue in
 CC the variant differs in no more than 15% of the amino acid residue of
 CC NOVX. Also included are an isolated nucleic acid (NA) molecule
 CC (comprising a nucleic acid sequence encoding a NOVX polypeptide above
 CC (odd SEQ ID NOS between ADG39769 and ADG39801), a nucleic acid fragment
 CC encoding at least a portion of a NOVX polypeptide and a complement of
 CC NOVX NA), a vector comprising NOVX NA, a cell comprising the vector, an
 CC antibody that immunospecifically binds to NOVX, a method for determining
 CC the presence or amount of NOVX or NOVX NA in a sample, a method for
 CC identifying an agent that binds to NOVX, a method for identifying an
 CC agent that modulates the expression or activity of NOVX, a method for
 CC modulating the activity of NOVX, a method for treating or preventing a
 CC NOVX-associated disorder, a method for screening for a modulator of
 CC activity or of latency or predisposition to a NOVX-associated disorder, a
 CC method for determining the presence of or predisposition to a disease
 CC associated with altered levels of NOVX or NOVX NA in a first mammalian
 CC subject and a method of treating a pathological state in a mammal by
 CC administering NOVX or an antibody that binds to NOVX. The NOVX
 CC polypeptide, nucleic acid or antibody is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease or a
 CC NOVX-associated disorder. The NOVX polypeptides and nucleic acids
 CC encoding them are useful for diagnosing or treating pathologies, diseases
 CC or conditions associated with NOVX sequences, including cardiomyopathy,
 CC atherosclerosis, hypertension, congenital heart defects, pulmonary
 CC stenosis, scleroderma, obesity, metabolic disturbances associated with
 CC hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm,
 CC adenocarcinoma, fertility, haemophilia, graft versus host disease, AIDS,
 CC bronchial asthma, Crohn's disease, multiple sclerosis, infectious disease,
 CC disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease,
 CC or Parkinson's disease), immune disorders, haematopoietic disorders,
 CC dyslipidaemias, and wasting disorders associated with chronic diseases.
 CC The polypeptides can be used as immunogens to produce antibodies and as
 CC vaccines. The sequences may further be used in chromosome mapping,
 CC identifying individual from minute biological samples (tissue typing),
 CC and in forensic identification of a biological sample. The present
 CC sequence is a protein showing sequence similarity to a NOVX protein.
 XX
 SQ Sequence 1708 AA;

Query Match 100.0%; Score 1231; DB 7; Length 1708;
 Best Local Similarity 100.0%; Pred. No. 8e-88;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVHGFSQSWAWRACSVTCGKGIQRSLCNQPLPANGKPCQGSLEMRNCQNKPCFVD 60
 Db 600 QVHGFSQSWAWRACSVTCGKGIQRSLCNQPLPANGKPCQGSLEMRNCQNKPCFVD 659
 QY 61 GSWSEWSLWEECTRCGRGNQTRTCNPNPSVQHGRCPCGNVAEILMNCNIRPCPVHGAW 120
 Db 660 GSWSEWSLWEECTRCGRGNQTRTCNPNPSVQHGRCPCGNVAEILMNCNIRPCPVHGAW 719
 QY 121 SAWQPMGTCSESCGXTQTRARLCNPPPAFGSGYCDGAETQMVQCNERNCPHKGWATW 180
 Db 720 SAWQPMGTCSESCGXTQTRARLCNPPPAFGSGYCDGAETQMVQCNERNCPHKGWATW 779
 QY 181 ASWSACSVSCGGARQTRGCSDPVQY 208
 Db 780 ASWSACSVSCGGARQTRGCSDPVQY 807

RESULT 7
 ADG39840
 ID ADG39840 standard; protein; 1708 AA.
 XX
 AC ADG39840;
 XX
 DT 26-FEB-2004 (first entry)
 XX Protein similar to human NOV9 #1.
 DE Human; NOVX; cardiomyopathy; atherosclerosis; hypertension;
 KW congenital heart defect; pulmonary stenosis; scleroderma; obesity;
 KW

KW metabolic disturbance; obesity; transplantation; adrenoleukodystrophy;
 KW congenital adrenal hyperplasia; prostate cancer; diabetes;
 KW metabolic disorder; neoplasm; adenocarcinoma; fertility; haemophilia;
 KW graft versus host disease; AIDS; bronchial asthma; Crohn's disease;
 KW multiple sclerosis; infectious disease; anorexia;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia;
 KW wasting disorder.
 XX
 OS Homo sapiens.
 XX
 PN US2003203843-A1.
 XX
 PD 30-OCT-2003.
 XX
 PF 11-APR-2002; 2002US-00120801.
 XX
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 25-APR-2001; 2001US-0286392P.
 PR 03-MAY-2001; 2001US-0288344P.
 PR 16-MAY-2001; 2001US-0291241P.
 PR 14-SEP-2001; 2001US-0322284P.
 XX
 PA (PENA/) PENA C E A.
 PA (GUOX/) GUO X.
 PA (SHIM/) SHIMKETS R A.
 PA (PADI/) PADIGARU M.
 PA (KEKU/) KEKUDA R.
 PA (SPYT/) SPYTEK K A.
 PA (MEHR/) MEHRABAN F.
 PA (TOPP/) TOPPER J N.
 PA (MALY/) MALYANKAR U M.
 PA (WASS/) WASSERMAN S M.
 PA (EDIN/) EDINGER S R.
 PA (SMIT/) SMITHSON G.
 PA (GUNT/) GUNTHER E.
 PA (KOMU/) KOMUVES L.
 XX
 PI Pena CEA, Guo X, Shimkets RA, Padigaru M, Kekuda R, Spytek KA;
 PI Mehraban F, Topper JN, Malyankar UM, Wasserman SM, Edinger SR;
 PI Smithson G, Gunther E, Komuves L;
 XX
 DR WPI; 2003-900671/82.
 XX
 XX New NOVX polypeptides and nucleic acids, useful for diagnosing or
 PT treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma,
 PT obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or
 PT multiple sclerosis.
 XX
 PS Disclosure; SEQ ID NO 72; 215pp; English.

XX The invention relates to a new isolated polypeptide comprising an amino
 CC acid sequence selected from 17 fully defined human NOVX sequences (even
 CC SEQ ID NOS between ADG39770 and ADG39802), a mature form of the NOVX
 CC amino acid or a variant of NOVX, where one or more amino acid residue in
 CC the variant differs in no more than 15% of the amino acid residues of
 CC NOVX. Also included are an isolated nucleic acid (NA) molecule
 CC (comprising a nucleic acid sequence encoding a NOVX polypeptide above
 CC (odd SEQ ID NOS between ADG39769 and ADG39801), a nucleic acid fragment
 CC encoding at least a portion of a NOVX polypeptide and a complement of
 CC NOVX NA), a vector comprising NOVX NA, a cell comprising the vector, an
 CC antibody that immunospecifically binds to NOVX, a method for determining
 CC the presence or amount of NOVX or NOVX NA in a sample, a method of
 CC identifying an agent that binds to NOVX, a method for identifying an
 CC agent that modulates the expression or activity of NOVX, a method for
 CC modulating the activity of NOVX, a method for treating or preventing a
 CC NOVX-associated disorder, a method for screening for a modulator of
 CC activity or of latency or predisposition to a NOVX-associated disorder, a
 CC method for determining the presence of or predisposition to a disease
 CC associated with altered levels of NOVX or NOVX NA in a first mammalian
 CC subject and a method of treating a pathological state in a mammal by

CC administering NOVX or an antibody that binds to NOVX. The NOVX
 CC polypeptide, nucleic acid or antibody is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease or a
 CC NOVX-associated disorder. The NOVX polypeptides and nucleic acids
 CC encoding them are useful for diagnosing or treating pathologies, diseases
 CC or conditions associated with NOVX sequences, including cardiomyopathy,
 CC atherosclerosis, hypertension, congenital heart defects, pulmonary
 CC stenosis, scleroderma, obesity, metabolic disturbances associated with
 CC obesity, transplacental, adrenoleukodystrophy, congenital adrenal
 CC hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm,
 CC adenocarcinoma, fertility, haemophilia, graft versus host disease, AIDS,
 CC bronchial asthma, Crohn's disease, multiple sclerosis, infectious
 CC disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease,
 CC or Parkinson's disease), immune disorders, haematopoietic disorders,
 CC dyslipidaemias, and wasting disorders associated with chronic diseases.
 CC The polypeptides can be used as immunogens to produce antibodies and as
 CC vaccines. The sequences may further be used in chromosome mapping.
 CC identifying individual from minute biological samples (tissue typing),
 CC and in forensic identification of a biological sample. The present
 CC sequence is a protein showing sequence similarity to a NOVX protein.
 XX
 SQ Sequence 1708 AA;

Query Match 100.0%; Score 1231; DB 7; Length 1708;
 Best Local Similarity 100.0%; Pred. No. 8e-88;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVHGGFSQWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPKCGSDLEMRNCNKPCPVD 60
 Db 600 QVHGGFSQWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPKCGSDLEMRNCNKPCPVD 659
 QY 61 GSWSEWSLWECTRSCGNGTQTRTCNNPVSQHGRCPEGNVAILNCNTRPCFVHGAW 120
 Db 660 GSWSEWSLWECTRSCGNGTQTRTCNNPVSQHGRCPEGNVAILNCNTRPCFVHGAW 719
 QY 121 SAWQPMWTCSESCGKGTQTRARLNNPPAPFGSGYCDGAETQMVQCNERNCPHGWATW 180
 Db 720 SAWQPMWTCSESCGKGTQTRARLNNPPAPFGSGYCDGAETQMVQCNERNCPHGWATW 779

QY 181 ASWSACSVCSSGGRQRTGCSDPVQY 208
 Db 780 ASWSACSVCSSGGRQRTGCSDPVQY 807
 RESULT 8
 ID ABU12084
 AC ABU12084; protein; 1902 AA.
 AC ABU12084;
 XX 19-FEB-2003 (first entry)
 DE Human NOV25c CQ56914-03 protein SEQ ID 98.
 XX NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
 KW antilipemic; cytotatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease.
 XX Homo sapiens.
 OS
 XX W0200281625-A2.
 FN
 XX 17-OCT-2002.
 PD
 XX 03-APR-2002; 2002WO-US010366.
 PF
 XX 03-APR-2001; 2001US-0281086P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 06-APR-2001; 2001US-0282020P.

10-APR-2001; 2001US-0282930P.
 12-APR-2001; 2001US-0283444P.
 13-APR-2001; 2001US-0283512P.
 13-APR-2001; 2001US-0283657P.
 13-APR-2001; 2001US-0283678P.
 13-APR-2001; 2001US-0283710P.
 17-APR-2001; 2001US-0284234P.
 19-APR-2001; 2001US-0285325P.
 20-APR-2001; 2001US-0285381P.
 24-APR-2001; 2001US-0286068P.
 25-APR-2001; 2001US-0286292P.
 26-JUN-2001; 2001US-0296692P.
 26-JUN-2001; 2001US-0300883P.
 08-AUG-2001; 2001US-0311003P.
 13-AUG-2001; 2001US-0311973P.
 16-AUG-2001; 2001US-0312901P.
 14-SEP-2001; 2001US-0322283P.
 05-OCT-2001; 2001US-0327448P.
 31-DEC-2001; 2001US-0345734P.
 03-JAN-2002; 2002US-0345755P.
 04-FEB-2002; 2002US-0354391P.
 02-APR-2002; 2002US-00114153.

(CURA-) CURAGEN CORP.

Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
 Smithson G, Guo X, Gerlach V, Gasman SJ, Boldog FL, Li L;
 Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CM, Spyttek KA;
 Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
 Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
 Mazur A;

WPI; 2003-046862/04.
 N-PSDB; ABX56304.

New isolated NOVX polypeptide useful for treating cardiomyopathy,
 atherosclerosis, metabolic disorders, diabetes, obesity, infectious
 disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
 cancer.

Claim 1; Page 184; 425pp; English.

This invention describes novel polypeptides, termed NOVX which have
 antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
 neuroprotective, antiparkinsonian, antilipemic, cytotatic, nootropic,
 cardiant and immunomodulatory activity. The polypeptide and any
 antibodies generated from it are useful in the manufacture of a
 medicament for treating a syndrome associated with a human disease
 and portions of the polynucleotides encoding NOVX polypeptides are useful
 to map the location of NOVX genes on a chromosome, to identify
 individuals from minute biological samples, as DNA markers for
 restriction fragment length polymorphism (RFLP), and are useful to
 prepare polymerase chain reaction primers. The products of the invention
 can be used in gene therapy and for treating cardiomyopathy, metabolic
 disorders, diabetes, atherosclerosis, obesity, infectious disease,
 anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
 disease, immune disorders, haematopoietic disorders, and various
 dyslipidaemias, metabolic disturbances associated with obesity, metabolic
 syndrome X and wasting disorders associated with chronic diseases and
 various cancers. ABU12041-ABU12086 represent the polypeptide fragments
 encoded by the NOVX polynucleotides represented in ABX56261-ABX56306

Sequence 1902 AA;

Query Match 100.0%; Score 1231; DB 6; Length 1902;
 Best Local Similarity 100.0%; Pred. No. 9e-88;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVHGGFSQWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPKCGSDLEMRNCNKPCPVD 60
 Db 911 QVHGGFSQWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPKCGSDLEMRNCNKPCPVD 970

Qy 61 GSWSESLWEECTSCGRGQTRTCTNNPVSQHGRCPCGNAVEIIMCNIRPCPVHGAW 120
 Db 971 GSWSESLWEECTSCGRGQTRTCTNNPVSQHGRCPCGNAVEIIMCNIRPCPVHGAW 1030
 Qy 121 SAWPWTCTSCSGKGTQTRARLCNNPPAPFGSGYCDGABTQMVQCNERNCPHIGKWATW 180
 Db 1031 SAWPWTCTSCSGKGTQTRARLCNNPPAPFGSGYCDGABTQMVQCNERNCPHIGKWATW 1090
 Qy 181 ASWSACSVSCGGARQTRCSDPVPQY 208
 Db 1091 ASWSACSVSCGGARQTRCSDPVPQY 1118
 RESULT 9
 ADH72108
 ID ADH72108 standard; protein; 1902 AA.
 XX AC ADH72108;
 XX DT 25-MAR-2004 (first entry)
 XX DE Human protein of the invention NOV43d SEQ ID NO:1004.
 KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
 KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.
 XX OS Homo sapiens.
 XX PN WC2003102155-A2.
 XX PD 11-DEC-2003.
 XX PF 03-JUN-2003; 2003WO-US017430.
 XX PR 03-JUN-2002; 2002US-0385120P.
 PR 04-JUN-2002; 2002US-0385784P.
 PR 05-JUN-2002; 2002US-0386041P.
 PR 06-JUN-2002; 2002US-0386047P.
 PR 06-JUN-2002; 2002US-0386376P.
 PR 06-JUN-2002; 2002US-0386453P.
 PR 06-JUN-2002; 2002US-0386864P.
 PR 07-JUN-2002; 2002US-0387016P.
 PR 07-JUN-2002; 2002US-0386798P.
 PR 07-JUN-2002; 2002US-0386816P.
 PR 07-JUN-2002; 2002US-0386931P.
 PR 07-JUN-2002; 2002US-0386942P.
 PR 07-JUN-2002; 2002US-0386971P.
 PR 07-JUN-2002; 2002US-0387262P.
 PR 08-JUN-2002; 2002US-0296960P.
 PR 10-JUN-2002; 2002US-0387400P.
 PR 10-JUN-2002; 2002US-0387535P.
 PR 11-JUN-2002; 2002US-0387610P.
 PR 11-JUN-2002; 2002US-0387625P.
 PR 11-JUN-2002; 2002US-0387634P.
 PR 11-JUN-2002; 2002US-0387669P.
 PR 11-JUN-2002; 2002US-0387696P.
 PR 11-JUN-2002; 2002US-0387702P.
 PR 11-JUN-2002; 2002US-0387836P.
 PR 11-JUN-2002; 2002US-0387859P.
 PR 12-JUN-2002; 2002US-0387933P.
 PR 12-JUN-2002; 2002US-0387934P.
 PR 12-JUN-2002; 2002US-0387960P.
 PR 12-JUN-2002; 2002US-0388022P.
 PR 12-JUN-2002; 2002US-0388095P.
 PR 13-JUN-2002; 2002US-0389123P.
 PR 14-JUN-2002; 2002US-0389118P.
 PR 14-JUN-2002; 2002US-0389120P.
 PR 14-JUN-2002; 2002US-0389144P.
 PR 14-JUN-2002; 2002US-0389146P.
 PR 17-JUN-2002; 2002US-0389729P.
 PR 17-JUN-2002; 2002US-0389742P.
 PR 18-JUN-2002; 2002US-0389864P.
 PR 19-JUN-2002; 2002US-0390006P.
 PR 21-JUN-2002; 2002US-0390209P.
 PR 21-JUN-2002; 2002US-0390763P.
 PR 17-JUL-2002; 2002US-0390706P.
 PR 06-AUG-2002; 2002US-0401628P.
 PR 09-AUG-2002; 2002US-0402156P.
 PR 09-AUG-2002; 2002US-0402256P.
 PR 09-AUG-2002; 2002US-0402389P.
 PR 12-AUG-2002; 2002US-0402786P.
 PR 12-AUG-2002; 2002US-0402816P.
 PR 12-AUG-2002; 2002US-0402821P.
 PR 13-AUG-2002; 2002US-0402832P.
 PR 13-AUG-2002; 2002US-0403448P.
 PR 13-AUG-2002; 2002US-0403459P.
 PR 13-AUG-2002; 2002US-0403531P.
 PR 13-AUG-2002; 2002US-0403532P.
 PR 13-AUG-2002; 2002US-0403563P.
 PR 15-AUG-2002; 2002US-0403617P.
 PR 26-AUG-2002; 2002US-0406182P.
 PR 26-AUG-2002; 2002US-0406355P.
 PR 27-AUG-2002; 2002US-0406240P.
 PR 12-SEP-2002; 2002US-0410094P.
 PR 20-SEP-2002; 2002US-0412528P.
 PR 23-SEP-2002; 2002US-0412731P.
 PR 30-SEP-2002; 2002US-0414801P.
 PR 30-SEP-2002; 2002US-0414839P.
 PR 30-SEP-2002; 2002US-0414840P.
 PR 30-SEP-2002; 2002US-0414954P.
 PR 09-OCT-2002; 2002US-0417186P.
 PR 09-OCT-2002; 2002US-0417406P.
 PR 23-OCT-2002; 2002US-0420639P.
 PR 28-OCT-2002; 2002US-0421156P.
 PR 31-OCT-2002; 2002US-0422590P.
 PR 01-NOV-2002; 2002US-0423130P.
 PR 05-NOV-2002; 2002US-00423798.
 PR 05-NOV-2002; 2002US-0423798P.
 PR 12-NOV-2002; 2002US-0425453P.
 (CURA-) CURAGEN CORP.
 PI Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
 PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
 PI Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
 PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
 PI MacLachlan T, Malvankar UM, Mezick AJ, Millet I, Mishra VS;
 PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raba D, Rastelli L;
 PI Riegler DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
 PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
 PI Zhong H;
 XX WPI; 2004-081935/08.
 DR N-PSDB; ADH72107.
 XX PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX Example 43; SEQ ID NO 1004; 1880pp; English.
 XX The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytostatic, immunomodulator,
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in a human disease. The
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious

CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC represents a NOVX polypeptide of the invention.

XX Sequence 1902 AA;

Query Match 100.0%; Score 1231; DB 8; Length 1902;
 Best Local Similarity 100.0%; Pred. No. 9e-88;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVHGFSQSAWRACSVTCGKGIQKSRRLCNQPLPANGKPKCGSDLEMRNCKPCPVD 60
 Db 911 QVHGFSQSAWRACSVTCGKGIQKSRRLCNQPLPANGKPKCGSDLEMRNCKPCPVD 970
 QY 61 GSWSESLWEECTSCGRCNQTRTRTCNNPSVQHGRCPCGNAVEIIMCNIIRPCPVHGA 120
 Db 971 GSWSESLWEECTSCGRCNQTRTRTCNNPSVQHGRCPCGNAVEIIMCNIIRPCPVHGA 1030
 QY 121 SAMQPMGTCSGCGKGTQTRARLNNPPAFGGSYCDGAETQVQVCNERNCPHGWATW 180
 Db 1031 SAMQPMGTCSGCGKGTQTRARLNNPPAFGGSYCDGAETQVQVCNERNCPHGWATW 1090
 QY 181 ASWSACSVSCGGARQTRGCDPVPQY 208
 Db 1091 ASWSACSVSCGGARQTRGCDPVPQY 1118

RESULT 10

ABP60991

ID ABP60991 standard; protein; 5635 AA.

XX AC ABP60991;

DT 10-SEP-2002 (first entry)

XX DE Novel human protein. SEQ ID 78.

XX Human; cytosolic; vulnery; antiarteriosclerotic; antiparkinsonian;
 KW neurotropic; neuroprotective; immunosuppressive; haemostatic;
 KW antiinflammatory; cardiant; antiulcer; virucide; antithyroid;
 KW cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
 KW wound healing disorders; atherosclerosis; Parkinson's disease;
 KW Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
 KW inflammation; neoplastic disease; nervous system disorder;
 KW cardiovascular disorders; pancreatitis; respiratory disorder;
 KW hyperproliferation; systemic autoimmune disease; hyper-immunity;
 KW developmental abnormality; gastrointestinal ulceration; neuropathy;
 KW haematological disease; metabolic disease; sperm dysfunction;
 KW thyroid disorder; hypothyroidism; brain damage; colitis;
 KW cone photo-transduction deficiency; neurological disease; stroke;
 KW angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
 KW trachea; thymus; lymph node; muscular system; obesity; anorexia;
 KW growth abnormality; precocious puberty.

XX Homo sapiens.

OS WO200250105-A1.

XX PD 27-JUN-2002.

XX PF 17-DEC-2001; 2001WO-US049232.

XX PR 19-DEC-2000; 2000US-0256710P.

XX PR 20-DEC-2000; 2000US-0257048P.

XX PR 09-JAN-2001; 2001US-0260482P.

XX PR 30-JAN-2001; 2001US-0264922P.

XX PR 06-FEB-2001; 2001US-0266797P.

XX PR 19-MAR-2001; 2001US-0276988P.

XX PR 04-APR-2001; 2001US-0281535P.

XX PR 08-MAY-2001; 2001US-0289622P.

XX PA (SMIX) SMITHKLINE BEECHAM CORP.

PA (SMIX) SMITHKLINE BEECHAM PLC.

PA (GLAX) GLAXO GROUP LTD.

XX Agarwal P, Birkeland M, Cogswell JP, Kabnick KF, Lai Y;

XX Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;

XX WPI; 2002-508784/54.

XX N-PSDB; ABQ86156.

XX Secreted proteins and polynucleotides useful as vaccines for preventing

XX or treating various diseases e.g. cancer, wounds, atherosclerosis,

XX Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.

XX Claim 1(a); Page 285-297; 335pp; English.

XX The invention relates to an isolated polypeptide with signal sequences

XX which allow it to be secreted extracellularly or membrane associated. The

XX activity of polypeptides of the invention may be described as,

XX cytosolic, vulnery, antiarteriosclerotic, antiparkinsonian, neurotropic,

XX neuroprotective, immunosuppressive, haemostatic, antiinflammatory,

XX cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic,

XX and metabolic. Polypeptides and polynucleotides of the invention are

XX useful in the treatment, or as a vaccine in the prevention of, cancer,

XX wound healing disorders, infection, atherosclerosis, Parkinson's disease

XX and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,

XX inflammation, neoplastic diseases, nervous system related disorders and

XX cardiovascular disorders, pancreatitis, respiratory disorder,

XX hyperproliferation, systemic autoimmune disease, hyper-immunity,

XX developmental abnormality, gastrointestinal ulceration, neuropathy,

XX haematological diseases, metabolic diseases, sperm dysfunction, thyroid

XX disorders e.g. hypothyroidism, brain damages, colitis, cone photo-

XX transduction deficiency, diseases in the spinal cord, thyroid gland, heart,

XX trachea, thymus, lymph node and muscular system, obesity, anorexia,

XX growth abnormalities, and alleviation of precocious puberty. The

XX sequences given in records ABP60965-ABP61019 represent novel human

XX proteins of the invention

XX Sequence 5635 AA;

QY Query Match 100.0%; Score 1231; DB 5; Length 5635;

Db Best Local Similarity 100.0%; Pred. No. 2.6e-87;

QY Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVHGFSQSAWRACSVTCGKGIQKSRRLCNQPLPANGKPKCGSDLEMRNCKPCPVD 60

Db 4527 QVHGFSQSAWRACSVTCGKGIQKSRRLCNQPLPANGKPKCGSDLEMRNCKPCPVD 4586

QY 61 GSWSESLWEECTSCGRCNQTRTRTCNNPSVQHGRCPCGNAVEIIMCNIIRPCPVHGA 120

Db 4587 GSWSESLWEECTSCGRCNQTRTRTCNNPSVQHGRCPCGNAVEIIMCNIIRPCPVHGA 4646

QY 121 SAMQPMGTCSGCGKGTQTRARLNNPPAFGGSYCDGAETQVQVCNERNCPHGWATW 180

Db 4647 SAMQPMGTCSGCGKGTQTRARLNNPPAFGGSYCDGAETQVQVCNERNCPHGWATW 4706

QY 181 ASWSACSVSCGGARQTRGCDPVPQY 208

Db 4707 ASWSACSVSCGGARQTRGCDPVPQY 4734

RESULT 11

ADU70089

ID ADU70089 standard; protein; 5636 AA.

XX AC ADU70089;

XX DT 06-MAY-2004 (first entry)

XX Human heat mitochondrial protein as a therapeutic target SeqID1895.

XX mitochondrial; human; screening assay; diabetes mellitus;

XX Huntington's disease; osteoarthritis;

XX

KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fiber syndrome; MERRF; cancer;
 KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 OS Homo sapiens.
 XX WO20003087768-A2.
 XX PD 23-OCT-2003.
 XX PF 04-APR-2003; 2003WO-US010870.
 XX PR 12-APR-2002; 2002US-0372843P.
 XX PR 17-JUN-2002; 2002US-0389987P.
 XX PR 20-SEP-2002; 2002US-0412418P.
 XX PA (MITO-) MITOKOR.
 XX PA (BUCK-) BUCK INST AGE RES.
 XX GHOSH SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX WPI; 2003-845369/78.
 PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX Claim 1; SEQ ID NO 1895; 180pp; English.
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fiber syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nontropic, antidiabetic, and
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX SQ Sequence 5636 AA;
 Query Match 100.0%; Score 1231; DB 7; Length 5636;
 Best Local Similarity 100.0%; Pred. No. 2.6e-87;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVHGFQSNWRAVCSVTGKGIQKRLCNQPLFANGKFCQGSQDLERNQCNKPCPD 60
 DB 4528 QVHGFQSNWRAVCSVTGKGIQKRLCNQPLFANGKFCQGSQDLERNQCNKPCPD 4587
 QY 61 GSWSEWSLWECTRCGNGNTRTTCNNPSVQHGRCCEGNVETTCNRPVHGAW 120
 DB 4598 GSWSEWSLWECTRCGNGNTRTTCNNPSVQHGRCCEGNVETTCNRPVHGAW 4647
 QY 121 SAWQPMGTCSCGKGTQTRARLNCNPPPAFGSGYCDGAETQMCVNERNCPIHGKATW 180
 DB 4648 SAWQPMGTCSCGKGTQTRARLNCNPPPAFGSGYCDGAETQMCVNERNCPIHGKATW 4707
 QY 181 ASWSACSVSCGGARQTRGCDPVPQY 208
 DB 4708 ASWSACSVSCGGARQTRGCDPVPQY 4735
 RESULT 12

ADJ83137
 ID ADJ83137 standard; protein; 5636 AA.
 XX AC ADJ83137;
 XX DT 06-MAY-2004 (first entry)
 XX DE Human hemocentin protein - SEQ ID 128.
 XX KW NOVX; cytostatic; antiarteriosclerotic; antidiabetic; antiasthmatic;
 KW antiallergic; antiinflammatory; respiratory; antiarthritic;
 KW dermatological; antibacterial; cerebroprotective; vasotropic; cardiant;
 KW haemostatic; hypotensive; hepatotropic; neuroprotective; anorectic;
 KW nontropic; antitumor; muscular; immunosuppressive; gynaecological;
 KW antipsoriatic; endocrine; ophthalmological; osteopathic;
 KW antiparkinsonian; anticonvulsant; tranquiliser; analgesic; nephrotropic;
 KW antifertility; antilipemic; cardiomyopathy; atherosclerosis; diabetes;
 KW cell signal processing; metabolic pathway; asthma; allergy; emphysema;
 KW autoimmune; graft-versus-host; arthritis; cancer; stroke; haemophilia;
 KW obesity; Alzheimer's; pain; chromosome mapping; tissue typing; human;
 KW hemocentin.
 XX OS Homo sapiens.
 XX PN US2003170630-A1.
 XX PD 11-SEP-2003.
 XX PF 21-DEC-2001; 2001US-00032189.
 XX PR 21-DEC-2000; 2000US-0257495P.
 PR 22-DEC-2000; 2000US-0258171P.
 PR 20-FEB-2001; 2001US-0269940P.
 PR 08-MAR-2001; 2001US-0274192P.
 PR 22-MAR-2001; 2001US-0277826P.
 PR 29-MAR-2001; 2001US-0279840P.
 PR 11-APR-2001; 2001US-0282981P.
 PR 13-APR-2001; 2001US-0283656P.
 PR 31-JUL-2001; 2001US-0309247P.
 PR 10-AUG-2001; 2001US-0311754P.
 PR 17-AUG-2001; 2001US-0313331P.
 XX (ALSO/) ALSOBROOK J P.
 PA (TCHE/) TCHERNEV V T.
 PA (LIUX/) LIU X.
 PA (SPYT/) SPYTEK K A.
 PA (ZERH/) ZERHUSEN B D.
 PA (PATT/) PATTURAJAN M.
 PA (LEPL/) LEPLEY D M.
 PA (BURG/) BURGESS C B.
 PA (SHIM/) SHIMKETS R A.
 PA (GROS/) GROSSE W M.
 PA (SZEK/) SZEKERES E S.
 PA (VERN/) VERNET C A M.
 PA (LILL/) LI L.
 PA (CASM/) CASMAN S J.
 PA (BOLD/) BOLDOG F L.
 PA (GORM/) GORMAN L.
 PA (GANG/) GANGOLLI E A.
 PA (FERN/) FERNANDES E R.
 PA (RIEG/) RIEGER D K.
 PA (EDIN/) EDINGER S R.
 PA (GUNT/) GUNTHER E.
 PA (MILL/) MILLET I.
 PA (SCIO/) SCIORE P.
 PA (ELLE/) ELLERMAN K.
 PA (MACD/) MACDOUGALL J R.
 PA (SMIT/) SMITHSON G.
 XX Alsobrook JP, Tchernev VT, Liu X, Spytek KA, Zerhusen BD;
 PI Patturajan M, Lepley DM, Burgess CE, Shimkets RA, Grosse WM;
 PI Szekeres ES, Vernet CAM, Li L, Casman SJ, Boldog FL, Gorman L;
 PI Gangolli EA, Fernandes ER, Rieger DK, Edinger SR, Gunther E;

PI Millet I, Sciore P, Ellerman K, Macdougall JR, Smithson G;
 DR WPI; 2003-898249/82.
 XX
 PT New NOVX polypeptides and nucleic acid molecules, useful for diagnosing,
 PT preventing or treating NOVX-associated polypeptide disorder, e.g.
 PT cardiomyopathy, atherosclerosis, diabetes, cancer, Parkinson's disease or
 PT asthma.
 XX
 PS Disclosure; SEQ ID NO 128; 263pp; English.

XX The invention relates to a novel isolated NOVX polypeptide. The
 CC polypeptide demonstrates cytostatic, antiarteriosclerotic, antidiabetic,
 CC antiasthmatic, anti-allergic, anti-inflammatory, respiratory,
 CC antiarthritic, dermatological, antibacterial, cerebroprotective,
 CC vasotropic, cardiant, haemostatic, hypotensive, hepatotropic,
 CC neuroprotective, anorectic, nootropic, antitumor, muscular,
 CC immunosuppressive, gynaecological, antiparkinsonian, endocrine,
 CC ophthalmological, osteopathic, antiparkinsonian, anticonvulsant,
 CC tranquiliser, analgesic, nephrotropic, antifertility and antilipaeamic
 CC activities. The NOVX polypeptide, nucleic acid or antibody of the
 CC invention may be useful for treating or preventing a NOVX-associated
 CC disorder, such as cardiomyopathy, atherosclerosis, diabetes or a disorder
 CC related to cell signal processing and metabolic pathway modulation.
 CC Furthermore, the NOVX polypeptides may be useful for diagnosing, treating
 CC or preventing diseases such as asthma, allergies, emphysema, autoimmune
 CC disease, graft-versus-host disease, arthritis, cancer, stroke,
 CC haemophilia, obesity, Alzheimer's disease and pain. The nucleic acids may
 CC be used as hybridisation probes, in chromosome mapping, tissue typing,
 CC preventive medicine or pharmacogenomics. The current sequence is that of
 CC a protein of the invention which is related to human NOVX protein.

XX Sequence 5636 AA;
 SQ Query Match 100.0%; Score 1231; DB 7; Length 5636;
 Best Local Similarity 100.0%; Pred. No. 2.6e-87;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGFFSQWAWACSVTCGKIGKESRLCNQPLPANGKPCQGSLEMRNCQKPCPD 60
 Db 4528 QVHGFFSQWAWACSVTCGKIGKESRLCNQPLPANGKPCQGSLEMRNCQKPCPD 4587
 Qy 61 GSWSESLWEECTSCGRGNQTRTRTCNNPVSQHGGRPCGNAVEIIMCNIRPCPVHGW 120
 Db 4588 GSWSESLWEECTSCGRGNQTRTRTCNNPVSQHGGRPCGNAVEIIMCNIRPCPVHGW 4647
 Qy 121 SAWQPMGTCTSESCGKGTQTRARLCNNPPPAFGSGYCDGAETQVQVCNERNCPIHGKWATW 180
 Db 4648 SAWQPMGTCTSESCGKGTQTRARLCNNPPPAFGSGYCDGAETQVQVCNERNCPIHGKWATW 4707
 Qy 181 ASWSACSVSCGGARQTRGCDPVPQY 208
 Db 4708 ASWSACSVSCGGARQTRGCDPVPQY 4735

RESULT 13
 ID ADK60205 standard; protein; 5636 AA.
 XX AC ADK60205;
 XX DT 06-MAY-2004 (first entry)
 XX DE Angiogenesis differentially expressed protein GS-P29.
 KW vasotropic; antirheumatic; antiarthritic; hypotensive; antianginal;
 KW anti-inflammatory; cardiant; angiogenesis inhibitor; gene therapy;
 KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;
 KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;
 KW ovary hyperstimulation; psoriasis; endometriosis; restenosis;
 KW angioplasty; cicatrization; peripheral vascular disease; hypertension;
 KW vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;
 KW ischemia; angina; myocardial infarction; chronic heart disease;

KW cardiac congestion; macular degeneration; osteoporosis.
 XX OS Homo sapiens.
 XX PN FR2836687-A1.
 XX PD 05-SEP-2003.
 XX 11-APR-2002; 2002FR-00004546.
 XX 04-MAR-2002; 2002FR-00002717.
 XX (GENE-) GENE SIGNAL.
 XX (ALMA-) AL MAHMOOD S.
 XX Colin S, Schneider C, Al Mahmood S;
 WPI; 2004-013912/02.
 DR N-PSDB; ADK60455.
 XX Compositions for diagnosing, prognosing and treating angiogenic disorders
 PT including tumor vascularization and heart disease, comprise nucleic acid
 PT or polypeptide differentially expressed in angiogenesis.
 XX Claim 7; SEQ ID NO 81; 424pp; French.

XX The invention relates to a novel pharmaceutical composition active on
 CC angiogenesis comprising an endothelial cell nucleic acid whose expression
 CC is induced by an angiogenic factor and inhibited by an angiostatic agent
 CC or its complement or fragment, a polypeptide sequence encoded by the
 CC nucleic acid or its fragment, a molecule capable of inhibiting expression
 CC of the nucleic acid or a molecule which binds to the polypeptide
 CC sequence. The invention is used to diagnose, prognose or treat an
 CC angiogenic disorder in a mammal, particularly a human. The disorder is
 CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,
 CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,
 CC endometriosis associated with neovascularization, restenosis due to
 CC angioplasty, overproduction of tissue due to cicatrization, a peripheral
 CC vascular disease, hypertension, thrombophlebitis, ischemia, angina,
 CC aneurism, arterial restenosis, chronic heart disease, cardiac congestion or
 CC myocardial infarction, chronic heart disease, cardiac congestion or
 CC macular degeneration due to age or osteoporosis. This sequence
 CC corresponds to a protein encoded by a differentially expressed DNA used
 CC in the composition of the invention.

XX Sequence 5636 AA;
 SQ Query Match 100.0%; Score 1231; DB 8; Length 5636;
 Best Local Similarity 100.0%; Pred. No. 2.6e-87;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGFFSQWAWACSVTCGKIGKESRLCNQPLPANGKPCQGSLEMRNCQKPCPD 60
 Db 4528 QVHGFFSQWAWACSVTCGKIGKESRLCNQPLPANGKPCQGSLEMRNCQKPCPD 4587
 Qy 61 GSWSESLWEECTSCGRGNQTRTRTCNNPVSQHGGRPCGNAVEIIMCNIRPCPVHGW 120
 Db 4588 GSWSESLWEECTSCGRGNQTRTRTCNNPVSQHGGRPCGNAVEIIMCNIRPCPVHGW 4647
 Qy 121 SAWQPMGTCTSESCGKGTQTRARLCNNPPPAFGSGYCDGAETQVQVCNERNCPIHGKWATW 180
 Db 4648 SAWQPMGTCTSESCGKGTQTRARLCNNPPPAFGSGYCDGAETQVQVCNERNCPIHGKWATW 4707
 Qy 181 ASWSACSVSCGGARQTRGCDPVPQY 208
 Db 4708 ASWSACSVSCGGARQTRGCDPVPQY 4735

RESULT 14
 ID ADK60506 standard; protein; 5636 AA.
 XX AC ADK60506;

XX DT 06-MAY-2004 (first entry)

XX DE Angiogenesis differentially expressed protein GS-P29.

XX KW vasotrophic; anti-rheumatic; anti-arthritic; hypotensive; anti-anginal;

XX KW anti-inflammatory; cardiac; angiogenesis inhibitor; gene therapy;

XX KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;

XX KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;

XX KW ovary hyperstimulation; psoriasis; endometriosis; restenosis;

XX KW angioplasty; cicatrization; peripheral vascular disease; hypertension;

XX KW vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;

XX KW ischemia; angina; myocardial infarction; chronic heart disease;

XX KW cardiac congestion; macular degeneration; osteoporosis.

XX OS Homo sapiens.

XX FN FR2836686-A1.

XX PD 05-SEP-2003.

XX PF 04-MAR-2002; 2002FR-00002717.

XX PR 04-MAR-2002; 2002FR-00002717.

XX PA (GENE-) GENE SIGNAL.

XX PA (ALMA/) AL MAHMOOD S.

XX PI Colin S, Schneider C, Al Mahmood S;

XX DR WPI; 2004-013911/02.

XX DR N-PSDB; ADK60756.

XX PT Compositions containing nucleic acid or polypeptide differentially

XX PT expressed in angiogenesis are useful to diagnose, prognose and treat

XX PT angiogenic disorders including tumor vascularization and heart disease.

XX PS Claim 7; SEQ ID NO 81; 405pp; French.

XX CC The invention relates to a novel pharmaceutical composition active on

XX CC angiogenesis comprising an endothelial cell nucleic acid whose expression

XX CC is induced by an angiogenic factor and inhibited by an angiostatic agent

XX CC or its complement or fragment, a polypeptide sequence encoded by the

XX CC nucleic acid or its fragment, a molecule capable of inhibiting expression

XX CC of the nucleic acid or a molecule which binds to the polypeptide

XX CC sequence. The invention is used to diagnose, prognose or treat an

XX CC angiogenic disorder in a mammal, particularly a human. The disorder is

XX CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,

XX CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,

XX CC endometriosis associated with neovascularization, restenosis due to

XX CC angioplasty, overproduction of tissue due to cicatrization, a peripheral

XX CC vascular disease, hypertension, vascular inflammation, Raynaud disease,

XX CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,

XX CC myocardial infarction, chronic heart disease, cardiac congestion or

XX CC macular degeneration due to age or osteoporosis. This sequence

XX CC corresponds to a protein encoded by a differentially expressed DNA used

XX CC in the composition of the invention.

XX SQ Sequence 5636 AA;

Query Match 100.0%; Score 1231; DB 8; Length 5636;

Best Local Similarity 100.0%; Pred. No. 2.6e-87;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVHGFSQSAWRACSVTCGKIQKRSRLCNPLPANGKPKCGSDLEMRNCKNPKCPVD 60

DB 4528 QVHGFSQSAWRACSVTCGKIQKRSRLCNPLPANGKPKCGSDLEMRNCKNPKCPVD 4587

QY 61 GSWSEWSLWEECTRCGRGNQTRTRTCNNPSVQHGRRPCEGNAVEIIMCNIRPCPVHGAW 120

DB 4588 GSWSEWSLWEECTRCGRGNQTRTRTCNNPSVQHGRRPCEGNAVEIIMCNIRPCPVHGAW 4647

QY 121 SAWQPMGTCSESCGKGTQTRARLCNNPPPAFGGSVCDGAETQMVQCNERNCPHKGWATW 180

DB 4648 SAWQPMGTCSESCGKGTQTRARLCNNPPPAFGGSVCDGAETQMVQCNERNCPHKGWATW 4707

QY 181 ASWSACSVCSCGGARQRTGCSDFVPQY 208

DB 4708 ASWSACSVCSCGGARQRTGCSDFVPQY 4735

RESULT 15

ADP73129

ID ADP73129 standard; protein; 5636 AA.

XX AC ADP73129;

XX DT 12-AUG-2004 (first entry)

XX DE Angiogenesis inhibitor human protein sequence, GS-P29.

XX KW Inhibitor; angiogenesis; antisense nucleic acid; immunisation;

XX KW angiogenic disorder; antiangiogenic; angiogenesis stimulator; cytostatic;

XX KW dermatological; antiarthritic; antirheumatic; anti-inflammatory;

XX KW vasotrophic; hypotensive; ophthalmological; antipsoriatic; cardiac;

XX KW gene therapy; antisense gene therapy; tumor vascularisation;

XX KW retinopathies; rheumatoid arthritis; Crohn's disease; atherosclerosis;

XX KW ovarian hyperstimulation; psoriasis; endometriosis; restenosis;

XX KW tissue granulation; peripheral vascular disorder; hypertension;

XX KW vascular inflammation; Raynaud's disease; aneurism; arterial restenosis;

XX KW thrombophlebitis; lymphadenopathy; lymphedema; ischaemia; angina;

XX KW myocardial infarction; chronic heart disease; congestive heart disease;

XX KW macular degeneration; human.

XX OS Homo sapiens.

XX FN FR2843753-A1.

XX PD 27-FEB-2004.

XX PF 20-JUN-2003; 2003FR-00007507.

XX PR 04-MAR-2002; 2002FR-00002717.

XX PA (GENE/) GENE S.

XX PA (ALMS/) AL M S.

XX PI Colin S, Schneider C, Al MS;

XX DR WPI; 2004-216677/21.

XX DR N-PSDB; ADP73078.

XX PT Antisense nucleic molecule useful as inhibitor of angiogenesis in the

XX PT treatment of angiogenic disorders, e.g., rheumatoid arthritis,

XX PT atherosclerosis and endometriosis.

XX PS Claim 1; SEQ ID NO 81; 404pp; French.

XX CC The invention relates to a novel inhibitor of angiogenesis comprising an

XX CC active substance chosen from at least one of a nucleic acid molecule, an

XX CC antisense nucleic acid molecule, a polypeptide or an antibody. The

XX CC invention further comprises: an antisense nucleic acid sequence chosen

XX CC from any of the sequences provided in the specification; preparation of an

XX CC antibody comprising in vivo or in vitro immunisation of an

XX CC immunocompetent animal cell, preferably of a vertebrate and most

XX CC preferably of a mammal, with at least one of the polypeptide sequences

XX CC chosen from a sequence provided in the specification; a mammalian

XX CC expression vector comprising at least one antisense sequence chosen from

XX CC an antisense nucleic acid provided in the specification; preparation of a

XX CC genetically modified cell, that over- or under-expresses a gene

XX CC implicated in an angiogenic disorder, comprising inserting the vector

XX CC from above into a mammalian cell; a genetically modified cell that over-

XX CC expresses or under-expresses at least one gene involved in angiogenesis

XX CC by a nucleic acid sequence chosen from any of ADP73049 to ADP73138, as in

XX CC the antisense nucleic acid selection of above, or a fragment of any of

XX CC these; preparation of a cell line that stably expresses an expression

CC vector. The angiogenesis inhibitor has the following activities:
 CC antiangiogenic, angiogenesis stimulator, angiogenesis inhibitor,
 CC cytostatic, dermatological, antiarthritic, antirheumatic,
 CC antiinflammatory, vasotropic, hypotensive, ophthalmological,
 CC antipsoriatic, and cardiant. The novel nucleic acid molecules of the
 CC invention may be used to treat disorders in gene therapy and antisense
 CC gene therapy. The nucleic acid sequences, proteins and antibodies as part
 CC of the therapeutic compositions are useful in treating a disorder of
 CC angiogenesis chosen from: tumour vascularisation, retinopathies,
 CC rheumatoid arthritis, Crohn's disease, atherosclerosis, ovarian
 CC hyperstimulation, psoriasis, endometriosis associated with
 CC neovascularisation, restenosis due to balloon angioplasty, tissue
 CC granulation due to scarification, peripheral vascular disorders,
 CC hypertension, vascular inflammation, Raynaud's disease, aneurism,
 CC arterial restenosis, thrombophlebitis, lymphadenopathy, lymphedema,
 CC ischaemia, angina, myocardial infarction, chronic heart disease,
 CC congestive heart disease, macular degeneration linked to age and
 CC osteoporosis. This sequence represents a human protein for the creation
 CC of an angiogenesis inhibitor of the invention.
 XX
 SQ Sequence 5636 AA;

Query Match 100.0%; Score 1231; DB 8; Length 5636;
 Best Local Similarity 100.0%; Pred. No. 2.6e-87;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QVHGGSQWAWRACSVTCGKIQKSRRLCNQPLPANGGKPCQGSDEMRNCQKPCPVD 60
 Db 4528 QVHGGSQWAWRACSVTCGKIQKSRRLCNQPLPANGGKPCQGSDEMRNCQKPCPVD 4587
 Qy 61 GSWSESLWEECTSCRGNGTTRTCNNPSPVOHGORPCGNAVELIMCNIRPCPVHGAW 120
 Db 4588 GSWSESLWEECTSCRGNGTTRTCNNPSPVOHGORPCGNAVELIMCNIRPCPVHGAW 4647
 Qy 121 SAMQPWGTCSESCGKGTQTRARLCNNPPPAFGGSYCDGAETQMVQCNERNCPHGWATW 180
 Db 4648 SAMQPWGTCSESCGKGTQTRARLCNNPPPAFGGSYCDGAETQMVQCNERNCPHGWATW 4707
 Qy 181 ASWSACSVSCGGARQTRCGSDPVPQY 208
 Db 4708 ASWSACSVSCGGARQTRCGSDPVPQY 4735

Search completed: November 17, 2004, 15:52:22
 Job time : 175 secs

OM protein - protein search, using sw model

Run on: November 17, 2004, 15:49:06 ; Search time 39 Seconds
(without alignments)

353.696 Million cell updates/sec

Title: US-10-019-065A-1
 Perfect score: 1231
 Sequence: 1 QVHGGSQSAWRACSVTCG.....SCGGARQTRGCSDPVQY 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/pdata1/1aa/5B_COMB.pcp: *
3: /cgn2_6/pdata1/1aa/6A_COMB.pcp: *
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/cgn2_6/pdata1/1aa/backfiles.pcp: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	511.5	41.6	939	4	US-09-854-845-16
2	511.5	41.6	954	4	US-09-854-845-14
3	511.5	41.6	1034	4	US-09-854-845-6
4	511.5	41.6	1049	4	US-09-854-845-2
5	511.5	41.6	1078	4	US-09-854-845-8
6	511.5	41.6	1093	4	US-09-854-845-4
7	511.5	41.6	1136	4	US-09-854-845-12
8	511.5	41.6	1151	4	US-09-854-845-10
9	495.5	40.3	441	3	US-08-985-536-3
10	488.5	39.7	1170	1	US-08-313-288B-20
11	478.5	39.7	1170	4	US-09-657-472-2
12	468.5	38.9	239	5	PCF-US93-01552-1
13	453	36.8	459	1	US-08-313-288B-15
14	453	36.8	1172	1	US-08-313-288B-19
15	417.5	33.9	788	2	US-08-918-914-4
16	398	32.3	479	4	US-09-270-767-46823
17	360	29.2	218	3	US-08-985-536-1
18	288.5	23.4	807	4	US-09-133-769-1
19	288.5	23.4	807	4	US-09-640-173-186
20	288.5	23.4	807	4	US-09-713-550-186
21	288.5	23.4	807	4	US-09-825-234-186
22	288.5	23.4	807	4	US-09-970-966-186
23	287.5	23.4	787	4	US-09-825-234-207
24	287.5	23.4	787	4	US-09-970-966-207
25	287.5	23.4	807	1	US-07-862-021B-10
26	287.5	23.4	807	1	US-08-313-288B-10
27	287.5	23.4	807	4	US-09-133-769-3

ALIGNMENTS

RESULT 1

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US-09-854-845-16
; Sequence 16, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 939
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-16

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Query Match . . . 41.6%; Score 511.5; DB 4; Length 939;

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581	PWTPMLPVNVITGGARQEQRFETCRAPLADPHGLQFGRRTTETRTCPADGSGSCDTDAL	640
116	-----VHGAWSAQNPNGTCSGCKGTQTQTARLCNNPPPAFGSSYCDGAET	161
641	VEDLLRSGSTSPHTVSGGWAAGPWSGSRDCELGFRVRKKTCTNPEPRNGGLPCVGDA	700
162	OMQVCNERCPTHGKWATWASACSVSQGGGARORTGCSDPVP	206
701	ETQDCNPQACPVRGAWSCWTSWSPSCSGGGHYQRTSCTSPAP	745

796 EYDCNPOACPVRGAWSCNTSWSPCSASCGGHHYORTRSC TSPAP 840

RESULT 5

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US-09-854-845-8
; Sequence 8, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. 6750054el Human S
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1078
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-8

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Query Match	41.6%	Score	511.5	DB 4;	Length	1078;			
Best Local Similarity	33.0%	Pred. No.	6.5e-35;						
Matches	94;	Conservative	22;	Mismatches	82;	Indels	87;	Gaps	3;
Qy	3	HGFSQSWAFACSVTCGKGIQKRSRLCNQPLPANGKPKQCGSDLEMRNC-QNKPKCPVDG	61						
Db	606	NGATPWSSWALCSTSCIGIGFQVQRSCSNAPRHGGRI CVKRSRERFNCNTEPCVPPI	665						
Qy	62	SWSWSLWEECTRSCGRGNQTRTTCNNPVSQHGRGRCBGNAVLICNIRPCP-----	115						
Db	666	FWASGWSKCSNCGGMGQRACEN-----GNSCLGCGVEFKTCNPGCCEVRNT	719						
Qy	116	-----	115						
Db	720	PWTPWLPVNVTTGGARQQRFRFTCRAPLADPHGLQFCRRRTETRTCPADGSGSCDTDAL	779						
Qy	116	-----VHGWSAWQPWGTCSESGKGTCTEARLCNNPPEAFGSSYCDGAET	161						
Db	780	VEDLLRSGSTSPHTVSGGWAAGWPMSSCSRDELGFVRKKTCTNPEPRNGGLPCVGDA	839						
Qy	162	QMQVCNERNCSITHGKWTAWSWASACSVSCGGGARQRTGCSDDVP	206						
Db	840	EVONCNPAQCPVRGWSCTWSWSPCASCGGHGYORTSCSTSPAP	894						

RESULT 6

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US-09-854-845-4
; Sequence 4, Application US/09854845
; Patent No. 6750054
;
; GENERAL INFORMATION:
;
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
;
; TITLE OF INVENTION: No. 6750054el Human S
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ IDS: 50
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 4
;
; LENGTH: 1093
;
; TYPE: PRT
;
; ORGANISM: homo sapiens
US-09-854-845-4
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Query Match	41.6%;	Score 511.5;	DB 4;	Length 1093;
Best Local Similarity	33.0%;	Pred. No. 6.6e-35;		
Matches	94;	Conservative	22;	Mismatches 82; Indels 87; Gaps 3;
Qy	3	HGFGSOWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPKQGSLSLEMRNC-QNKPCPVDG	61	
Db	606	NGAATFWSSWALCSTSCGIGFQVQRQSCSNPAPRHGGRIICVGKSREBFNCNTPCFVPI	665	
Qy	62	SNSEWSLWEECTSCGCGNQTETTCNNPSVQHGGRPCENAVELIINCNIKPCP-----	115	
Db	666	FWASGWSKSCSNCGGMSRRACN-----GNSCLCGVEFTCNPEGCEVERRNT	719	
Qy	116	-----	115	
Db	720	PWTPLPVNVTGGARQQRFRFTCRAPLADPHGLQFRRRTETRTCPADGSGSCDTDAL	779	
Qy	116	-----VHGAWAOWPWTGCSBSCGKGTOTRCLCNPPAPFAGGSGYCDGAET	161	
Db	780	VEDLLRSGTSPHTVSGGWAAPGWSSCSRDCELGFVRKRTCTNPRNGGLFCVGDA	839	
Qy	162	QMVCYNERNCPIHGKATWASWSACSVCGGGARQRTGCGSDPVP	206	
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RESULT 7

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US-09-854-845-12
; Sequence 12, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr
; TITLE OF INVENTION: No. 6750054el H
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/8
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/20505
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Versi
; SEQ ID NO 12
; LENGTH: 1136
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-12

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[illegible]

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DB 838 VEDLLRSGTSPHTVSGGAAWGPWSCSRDCELGFRVVKTKCTNPEFRNGGLPCVGDAA 897
QY 162 QMVCNERNCPHGWATWASWSACSVCSCGAGQRTGCGSDPVP 206
DB 898 EYQDCNPQACPRGAWSCWTSWSPCSASCGGHHYQRTSCTSPAP 942

RESULT 8
US-09-854-845-10
; Sequence 10, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; FILE REFERENCE: LEX-0177-USA
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; CURRENT APPLICATION NUMBER: US/09/854,845
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-10

Query Match 41.6%; Score 511.5; DB 4; Length 1151;
Best Local Similarity 33.0%; Pred. No. 7e-35;
Matches 94; Conservative 22; Mismatches 82; Indels 87; Gaps 3;

QY 3 HGGFQSWAARACSVTCGKGIQKRSRLCNQPLPANGKPCQGSLEMRNC-QNKPCPDVG 61
DB 664 NGATPWSSWALCSTSGTGFQVRQSCSNPAPRHGGRICVKGSRERFCNENPCFVPI 723
QY 62 SWSLSWECTSCGNGNTRTRTCNNPVSQHGSPCEGNAVEIIMCNIRPCP----- 115
DB 724 FWASGWSKSCSSCGGMSRRACEN-----GNSCLGCGVEFKTCNPEGCPVRNT 777
QY 116 ----- 115
DB 778 PWTPLPVNVTQGAQRQRFRTCTRAPLADPHLGQFGRRTTETRTCPADGSGCDTAL 837
QY 116 -----VHGASAWOPWGTCSGKGTQTRARLCNNPPPPAFGGSYCDGAET 161
DB 838 VEDLLRSGTSPHTVSGGAAWGPWSCSRDCELGFRVVKTKCTNPEFRNGGLPCVGDAA 897
QY 162 QMVCNERNCPHGWATWASWSACSVCSCGAGQRTGCGSDPVP 206
DB 898 EYQDCNPQACPRGAWSCWTSWSPCSASCGGHHYQRTSCTSPAP 942

RESULT 9
US-09-855-526-3
; Sequence 3, Application US/09895526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
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; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-985-526-3

Query Match 40.3%; Score 495.5; DB 3; Length 441;
Best Local Similarity 30.5%; Pred. No. 5.7e-34;
Matches 93; Conservative 31; Mismatches 72; Indels 109; Gaps 5;

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DB 136 GGWHSWFSWSSCVTCGDGVITRITLCNPSPPQNGKPCGEARETRKACKDACPINGGW 195
QY 64 SEMSLWECTSCGNGNTRTRTC-----NN----- 89
DB 196 GWPSPWDICSVTCGGVQKSRCLVDSEMTENKELANERPLCYHNGVQVRNNEWT 255
QY 90 -----PS----- 91
DB 256 VDSCTECHCONSVTICKKVCIPMPCSNATVPDGECCPCWPSDSADDDGWSWSEWTS 315
QY 92 -----VOHGRP-----CEGNAVEIIMCNIRPCPVH-----GAKSAPWGTCSG 134
DB 316 TSCNGICQGRSCDSLNNRCSSSVOTRTCHIQCDKRFKQGGHWSWSSCVTCG 375
QY 135 KGQTRARLCNNPPPPAFGGSYCDGAETQMVQCNERNCPHGWATWASWSACSVCSCGGA 194
DB 376 DGVITRITLCNPSPPQNGKPCGEARETRKACKDACPINGGWGWPSPWDICSVTCGGV 435
QY 195 RQRT 199
DB 436 QKRSR 440

RESULT 10
US-08-313-288B-20
; Sequence 20, Application US/08313288B
; Patent No. 5750502
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M. and Avihu Klar
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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, CURRENT APPLICATION DATA:
 , APPLICATION NUMBER: PCT/US93/01652
 , FILING DATE: 19930222
 , CLASSIFICATION:
 , PRIOR APPLICATION DATA:
 , APPLICATION NUMBER: US/07/841,656
 , FILING DATE: 24-FEB-1992
 , PRIOR APPLICATION DATA:
 , APPLICATION NUMBER: US/07/464,369
 , FILING DATE: 12-JAN-1990
 , ATTORNEY/AGENT INFORMATION:
 , NAME: Pentress, Susan B.
 , REGISTRATION NUMBER: 31,327
 , REFERENCE/DOCKET NUMBER: 92005-PCT
 , TELECOMMUNICATION INFORMATION:
 , TELEPHONE: (312)-456-8000
 , TELEFAX: (312)-456-7776
 , INFORMATION FOR SEQ ID NO: 1:
 , SEQUENCE CHARACTERISTICS:
 , LENGTH: 239 amino acids
 , TYPE: AMINO ACID
 , STRANDEDNESS: unknown
 , TOPOLOGY: unknown
 , MOLECULE TYPE: peptide
 , PCT-US93-01652-1

Query Match 38.9%; Score 478.5; DB 5; Length 239;
 Best Local Similarity 46.9%; Pred. No. 8.1e-33;

Patent No. 5876963
GENERAL INFORMATION:
APPLICANT: Mitchell, Peter
APPLICANT: Hutchinson, Nancy
APPLICANT: Lawton, Michael
APPLICANT: Magna, Holly
APPLICANT: Yocum, Sue
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHOSPHORYLASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,914
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0369
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1070094
US-08-918-914-4

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Db 454 VSGVHWDSDWSTCSTCGDGAKSRRECEST-----NNCOGADYETPCNLGFCQ--- 503
QY 62 SWSLWEECTRCGRGNQTRTRTCNNPNSVOHGRPCEGNAVEIMCNIRPCPVHGWS 121
Db 504 TWSEWCWSTCSASCGSGQRERTRFCH-----LGTNRCEKDYSESEQCSAGFCP---EWS 555
QY 122 ANQPMWTCSESGKGTQTARLNCNNPPAPFGGSGYCDGAETOMQVNCNERNCPHGWATWA 181
Db 556 QWEDWQCQSVTCQGVAVNQRCTCLG--GVFGHLCOGPKTEQRACDGGFCSL---WSPWQ 610
QY 182 SWSACSVSCGGGARQTRGC 201
Db 611 EWSACSASCGSGMKRRQRCV 630

Search completed: November 17, 2004, 15:57:03
Job time: 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2004, 15:52:32 ; Search time 140 seconds
(without alignments)
525.132 Million cell updates/sec

Title: US-10-019-065A-1

Perfect score: 1231

Sequence: 1 QVHGFQSAWRACSVTCG.....SCGGARQTRGCSDPVQY 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.rep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.rep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.rep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.rep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.rep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1231	100.0	208	15	US-10-019-065A-1
2	1231	100.0	707	15	US-10-138-588-18
3	1231	100.0	1336	15	US-10-019-065A-33
4	1231	100.0	1902	14	US-10-114-153-88
5	1231	100.0	3645	14	US-10-120-801-73
6	1231	100.0	5635	15	US-10-451-168-78
7	1231	100.0	5636	14	US-10-032-189-128
8	1231	100.0	5636	14	US-10-120-801-72
9	1231	100.0	5636	14	US-10-023-634-93
10	1231	100.0	5636	16	US-10-408-765A-1895
11	1230	99.9	2572	14	US-10-114-153-86
12	1230	99.9	2673	14	US-10-120-801-76
13	1230	99.9	3645	14	US-10-032-189-127

14	1230	99.9	4495	15	US-10-138-588-20	Sequence 20, Appl
15	1169	95.0	197	15	US-10-019-065A-31	Sequence 31, Appl
16	852	69.2	634	15	US-10-115-479-86	Sequence 86, Appl
17	648	52.6	1953	15	US-10-115-479-88	Sequence 88, Appl
18	644	52.3	877	9	US-09-764-898-200	Sequence 200, Appl
19	633	51.4	800	9	US-09-764-898-124	Sequence 124, Appl
20	633	51.4	800	9	US-09-764-898-272	Sequence 272, Appl
21	633	51.4	800	9	US-10-073-865-124	Sequence 124, Appl
22	633	51.4	800	14	US-10-190-115-43	Sequence 43, Appl
23	533.5	43.3	1077	15	US-10-369-072-43	Sequence 43, Appl
24	533.5	43.3	1077	15	US-10-190-115-44	Sequence 44, Appl
25	522.5	42.4	1074	14	US-10-369-072-44	Sequence 44, Appl
26	522.5	42.4	1074	15	US-10-190-115-41	Sequence 41, Appl
27	520.5	42.3	1074	14	US-10-369-072-41	Sequence 41, Appl
28	520.5	42.3	1074	15	US-10-019-065A-32	Sequence 32, Appl
29	519.5	42.2	194	15	US-10-225-567A-342	Sequence 342, Appl
30	519.5	42.2	1584	14	US-10-190-115-116	Sequence 116, Appl
31	511.5	41.6	401	14	US-09-854-845-16	Sequence 16, Appl
32	511.5	41.6	939	9	US-09-854-845-14	Sequence 14, Appl
33	511.5	41.6	954	9	US-09-854-845-2	Sequence 2, Appl
34	511.5	41.6	1034	9	US-09-854-845-8	Sequence 8, Appl
35	511.5	41.6	1049	9	US-09-854-845-4	Sequence 4, Appl
36	511.5	41.6	1078	9	US-10-102-524-1858	Sequence 1858, Ap
37	511.5	41.6	1093	14	US-10-190-115-106	Sequence 106, Appl
38	511.5	41.6	1093	14	US-10-190-115-108	Sequence 108, Appl
39	511.5	41.6	1130	14	US-09-854-845-12	Sequence 12, Appl
40	511.5	41.6	1136	9	US-10-102-524-1857	Sequence 1857, Ap
41	511.5	41.6	1151	9	US-10-102-524-1856	Sequence 1856, Ap
42	511.5	41.6	1151	14	US-10-190-115-45	Sequence 45, Appl
43	511.5	41.6	1202	14		
44	511.5	41.6				
45	511.5	41.6				

ALIGNMENTS

RESULT 1
US-10-019-065A-1
; Sequence 1, Application/US/10019065A
; Publication No. US20040086501A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Corporation
; TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
; FILE REFERENCE: MSB-7265-PCT
; CURRENT APPLICATION NUMBER: US/10/019,065A
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/266,300
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-019-065A-1

Query Match	100.0%	Score 1231;	DB 15;	Length 208;
Best Local Similarity	100.0%	Pred. No. 7.6e-93;		
Matches 208;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	QVHGFQSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGS	DLERNQCNKPCFVD	60
Db	1	QVHGFQSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGS	DLERNQCNKPCFVD	60
Qy	61	GSWSLSLWBECTSCRGNGQTRTRTCNNPSVQHGGRPCGNAVEIIMCNRIRPCFVHGA	120	
Db	61	GSWSLSLWBECTSCRGNGQTRTRTCNNPSVQHGGRPCGNAVEIIMCNRIRPCFVHGA	120	
Qy	121	SAWQPMGTCSBSCGKGIQTRARLNNPPAFGSGYCDGAETQMCVNCNRCPIHGKWA	180	
Db	121	SAWQPMGTCSBSCGKGIQTRARLNNPPAFGSGYCDGAETQMCVNCNRCPIHGKWA	180	

Qy 181 ASWSACSVSCGGARQTRGCSDPVPOY 208
|
Db 181 ASWSACSVSCGGARQTRGCSDPVPOY 208

RESULT 2

US-10-138-588-18
; Sequence 18, Application US/10138588
; Publication No. US20040018594A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACID
; FILE REFERENCE: 21402-347A
; CURRENT APPLICATION NUMBER: US/10/138,588
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/288,395
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/308,901
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,388
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/324,757
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/288,900
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 203
; SEQ ID NO 18
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-588-18

Query Match 100.0%; Score 1231; DB 15; Length 707;
Best Local Similarity 100.0%; Pred. No. 2.3e-92;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGFSQSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDEMRNCKPKCPVD 60
|
Db 471 QVHGFSQSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDEMRNCKPKCPVD 530
|
Qy 61 GSWSESLWEECTSCGRGNQTRTTCNNPSVQHGGRPCGNAVEIIMCNIIRPCPVHGAW 120
|
Db 531 GSWSESLWEECTSCGRGNQTRTTCNNPSVQHGGRPCGNAVEIIMCNIIRPCPVHGAW 590
|
Qy 121 SAWQPMGTCSGKGTQTRARLCNNPPPAFGSGYCDGAETQMVQVNCNRCPIHGKWATW 180
|
Db 591 SAWQPMGTCSGKGTQTRARLCNNPPPAFGSGYCDGAETQMVQVNCNRCPIHGKWATW 650
|
Qy 181 ASWSACSVSCGGARQTRGCSDPVPOY 208
|
Db 651 ASWSACSVSCGGARQTRGCSDPVPOY 678

RESULT 3

US-10-019-065a-33
; Sequence 33, Application US/10019065A
; Publication No. US20040086501A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Corporation
; TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
; FILE REFERENCE: MSB-7265-PCT
; CURRENT APPLICATION NUMBER: US/10/019,065A
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/266,300
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 33
; LENGTH: 1336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-019-065a-33

Query Match 100.0%; Score 1231; DB 15; Length 1336;
Best Local Similarity 100.0%; Pred. No. 4.2e-92;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGFSQSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDEMRNCKPKCPVD 60
|
Db 654 QVHGFSQSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDEMRNCKPKCPVD 713
|
Qy 61 GSWSESLWEECTSCGRGNQTRTTCNNPSVQHGGRPCGNAVEIIMCNIIRPCPVHGAW 120
|
Db 714 GSWSESLWEECTSCGRGNQTRTTCNNPSVQHGGRPCGNAVEIIMCNIIRPCPVHGAW 773
|
Qy 121 SAWQPMGTCSGKGTQTRARLCNNPPPAFGSGYCDGAETQMVQVNCNRCPIHGKWATW 180
|
Db 774 SAWQPMGTCSGKGTQTRARLCNNPPPAFGSGYCDGAETQMVQVNCNRCPIHGKWATW 833
|
Qy 181 ASWSACSVSCGGARQTRGCSDPVPOY 208
|
Db 834 ASWSACSVSCGGARQTRGCSDPVPOY 861

RESULT 4

US-10-114-153-88
; Sequence 88, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Sheroy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennnda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Perenc
; APPLICANT: Li, Li
; APPLICANT: Zethusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malvankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACID
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657

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; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 88
; LENGTH: 1902
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-153-88

Query Match      100.0%; Score 1231; DB 14; Length 1902;
Best Local Similarity 100.0%; Pred. No. 5.9e-92;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVHGFQSAWRAACSVTCGKGIQKRSRLCNQPLPANGGKPCQGSDEMRNCQKPCPD 60
Db 911 QVHGFQSAWRAACSVTCGKGIQKRSRLCNQPLPANGGKPCQGSDEMRNCQKPCPD 970
QY 61 GSWSESLWEECTRCGRNQTRTRTCNNPSPVQHGGRPCGNAVEIIMCNIIRPCPVHGA 120
Db 971 GSWSESLWEECTRCGRNQTRTRTCNNPSPVQHGGRPCGNAVEIIMCNIIRPCPVHGA 1030
QY 121 SAWPMTGTCSECGKGTQTRARLCNNPPAFGGSYCDGAETQMVQCNERNCPHKGKATW 180
Db 1031 SAWPMTGTCSECGKGTQTRARLCNNPPAFGGSYCDGAETQMVQCNERNCPHKGKATW 1090
QY 181 ASWSACSVSCGGGARQTRGCDPVPQY 208
Db 1091 ASWSACSVSCGGGARQTRGCDPVPQY 1118

RESULT 5
US-10-120-801-73
; Sequence 73, Application US/10120801
; Publication No. US20030203843A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Mehraban, Fuad
; APPLICANT: Topper, James N.
; APPLICANT: Malyankar, Uriel
; APPLICANT: Wasserman, Scott
; APPLICANT: Edinger, Shlomit
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Komuves, Laszlo
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCES: 21402-340
; CURRENT APPLICATION NUMBER: US/10/120,801
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/285748
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 60/286068
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/286292
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/288334
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/291241
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/322284
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/285609
; PRIOR FILING DATE: 2001-04-20
```

```
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 3645
; TYPE: PRT
; ORGANISM: human
US-10-120-801-73

Query Match      100.0%; Score 1231; DB 14; Length 3645;
Best Local Similarity 100.0%; Pred. No. 1.1e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVHGFQSAWRAACSVTCGKGIQKRSRLCNQPLPANGGKPCQGSDEMRNCQKPCPD 60
Db 2537 QVHGFQSAWRAACSVTCGKGIQKRSRLCNQPLPANGGKPCQGSDEMRNCQKPCPD 2596
QY 61 GSWSESLWEECTRCGRNQTRTRTCNNPSPVQHGGRPCGNAVEIIMCNIIRPCPVHGA 120
Db 2597 GSWSESLWEECTRCGRNQTRTRTCNNPSPVQHGGRPCGNAVEIIMCNIIRPCPVHGA 2656
QY 121 SAWPMTGTCSECGKGTQTRARLCNNPPAFGGSYCDGAETQMVQCNERNCPHKGKATW 180
Db 2657 SAWPMTGTCSECGKGTQTRARLCNNPPAFGGSYCDGAETQMVQCNERNCPHKGKATW 2716
QY 181 ASWSACSVSCGGGARQTRGCDPVPQY 208
Db 2717 ASWSACSVSCGGGARQTRGCDPVPQY 2744

RESULT 6
US-10-451-168-78
; Sequence 78, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 5635
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-168-78

Query Match      100.0%; Score 1231; DB 15; Length 5635;
Best Local Similarity 100.0%; Pred. No. 1.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVHGFQSAWRAACSVTCGKGIQKRSRLCNQPLPANGGKPCQGSDEMRNCQKPCPD 60
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Db 4527 QVHGFSQSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDLERNCONKPCPVD 4586
QY 61 GSWSESLWEECTSCGRGNOTRTTCNNPVSQVHGGPRCEGNAVEIIMCNIRPCPVHGAW 120
Db 4587 GSWSESLWEECTSCGRGNOTRTTCNNPVSQVHGGPRCEGNAVEIIMCNIRPCPVHGAW 4646
QY 121 SAWPWTCTSESCKGQTQTRARLNCNNPPAFGSGYCDGAEQTMQVNCNERNCPHKGWATW 180
Db 4647 SAWPWTCTSESCKGQTQTRARLNCNNPPAFGSGYCDGAEQTMQVNCNERNCPHKGWATW 4706
QY 181 ASWSACSVSCGGARQTRGSDVPVQY 208
Db 4707 ASWSACSVSCGGARQTRGSDVPVQY 4734

RESULT 7

US-10-032-189-128
; Sequence 128, Application US/10032189
; Publication No. US20030170630A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard A
; APPLICANT: Grosse, William M
; APPLICANT: Szekeres, Edward S
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Gorman, Linda
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Rieger, Daniel K
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-228
; CURRENT APPLICATION NUMBER: US/10/032,189
; CURRENT FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/257,495
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/258,171
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/269,940
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/274,192
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/277,826
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/279,840
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/282,981
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/283,656
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/309,247
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/311,754
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,331
; PRIOR FILING DATE: 2001-08-17

; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 5636
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3003)
; OTHER INFORMATION: Wherein Xaa is any amino acid.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3041)
; OTHER INFORMATION: Wherein Xaa is any amino acid.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3367)
; OTHER INFORMATION: Wherein Xaa is any amino acid.
US-10-032-189-128
Query Match 100.0%; Score 1231; DB 14; Length 5636;
Best Local Similarity 100.0%; Pred. No. 1.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVHGFSQSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDLERNCONKPCPVD 60
Db 4528 QVHGFSQSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDLERNCONKPCPVD 4587
QY 61 GSWSESLWEECTSCGRGNOTRTTCNNPVSQVHGGPRCEGNAVEIIMCNIRPCPVHGAW 120
Db 4588 GSWSESLWEECTSCGRGNOTRTTCNNPVSQVHGGPRCEGNAVEIIMCNIRPCPVHGAW 4647
QY 121 SAWPWTCTSESCKGQTQTRARLNCNNPPAFGSGYCDGAEQTMQVNCNERNCPHKGWATW 180
Db 4648 SAWPWTCTSESCKGQTQTRARLNCNNPPAFGSGYCDGAEQTMQVNCNERNCPHKGWATW 4707
QY 181 ASWSACSVSCGGARQTRGSDVPVQY 208
Db 4708 ASWSACSVSCGGARQTRGSDVPVQY 4735
RESULT 8
US-10-120-801-72
; Sequence 72, Application US/10120801
; Publication No. US20030203843A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Mehraban, Fuad
; APPLICANT: Topper, James N.
; APPLICANT: Malyankar, Uriel
; APPLICANT: Wasserman, Scott
; APPLICANT: Edinger, Shlomit
; APPLICANT: Smithson, Glennda
; APPLICANT: Gunther, Erik
; APPLICANT: Komuves, Laszlo
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-340
; CURRENT APPLICATION NUMBER: US/10/120,801
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/285748
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 60/285068
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/286292
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/288334
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/291241

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; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/322284
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/285609
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 5636
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3003)
; OTHER INFORMATION: Wherein Xaa is any amino acid.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3041)
; OTHER INFORMATION: Wherein Xaa is any amino acid.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3367)
; OTHER INFORMATION: Wherein Xaa is any amino acid.
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 5636
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3003)
; OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
; OTHER INFORMATION: specification.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3041)
; OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
; OTHER INFORMATION: specification.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3367)
; OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
; OTHER INFORMATION: specification.
; US-10-023-634-93

Query Match      100.0%; Score 1231; DB 14; Length 5636;
Best Local Similarity 100.0%; Pred. No. 1.6e-91;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVHGFSQWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDDLEMRNCQKPCPVD 60
Db 4528 QVHGFSQWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDDLEMRNCQKPCPVD 4587

QY 61 GSSEWSLWEECTRS CGRGNQTRTRTCNNPVSQHGGRPCEGNAVEIIMCNIIRPCPVHGA 120
Db 4588 GSSEWSLWEECTRS CGRGNQTRTRTCNNPVSQHGGRPCEGNAVEIIMCNIIRPCPVHGA 4647

QY 121 SAWQPMGTCSGCGKTQTRARLNNPPPAFGSYCDGAETQMVQCNERNCPHKGKATW 180
Db 4648 SAWQPMGTCSGCGKTQTRARLNNPPPAFGSYCDGAETQMVQCNERNCPHKGKATW 4707

QY 181 ASWSACSVSCGGARQRTGCDPVPQY 208
Db 4708 ASWSACSVSCGGARQRTGCDPVPQY 4735

RESULT 9
US-10-023-634-93
; Sequence 93, Application US/10023634
; Publication No. US20030236389A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Colman, Steven D
; APPLICANT: Spytke, Kimberly A
; APPLICANT: Ballinger, Robert A
; APPLICANT: Quc, Xiaojia
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Li, Li
; APPLICANT: Ellerman, Karen
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gangolli, Esha A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Gerlach, Valerie

; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-221
; CURRENT APPLICATION NUMBER: US/10/023,634
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,025
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/265,163
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,929
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/274,864
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/276,688
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,880
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/286,409
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/309,246
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/315,600
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 5636
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3003)
; OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
; OTHER INFORMATION: specification.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3041)
; OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
; OTHER INFORMATION: specification.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3367)
; OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
; OTHER INFORMATION: specification.
; US-10-023-634-93

Query Match      100.0%; Score 1231; DB 14; Length 5636;
Best Local Similarity 100.0%; Pred. No. 1.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVHGFSQWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDDLEMRNCQKPCPVD 60
Db 4528 QVHGFSQWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDDLEMRNCQKPCPVD 4587

QY 61 GSSEWSLWEECTRS CGRGNQTRTRTCNNPVSQHGGRPCEGNAVEIIMCNIIRPCPVHGA 120
Db 4588 GSSEWSLWEECTRS CGRGNQTRTRTCNNPVSQHGGRPCEGNAVEIIMCNIIRPCPVHGA 4647

QY 121 SAWQPMGTCSGCGKTQTRARLNNPPPAFGSYCDGAETQMVQCNERNCPHKGKATW 180
Db 4648 SAWQPMGTCSGCGKTQTRARLNNPPPAFGSYCDGAETQMVQCNERNCPHKGKATW 4707

QY 181 ASWSACSVSCGGARQRTGCDPVPQY 208
Db 4708 ASWSACSVSCGGARQRTGCDPVPQY 4735

RESULT 10
US-10-408-765A-1895
; Sequence 1895, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
```

```

; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1895
; LENGTH: 5636
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: 3003, 3041, 3367
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-408-765A-1895

Query Match 100.0%; Score 1231; DB 16; Length 5636;
Best Local Similarity 100.0%; Pred. No. 1.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGFSQSAWRACSVTCGKGIQKSRCLNQLPANGKPKCGSDLEMRNCKPCPD 60
Db 4528 QVHGFSQSAWRACSVTCGKGIQKSRCLNQLPANGKPKCGSDLEMRNCKPCPD 4587

Qy 61 GSWSESLWEECTSCRGNGQTTRTCNNPSVOHGGRCBGNAVEIMCNIIRPCPVHGA 120
Db 4588 GSWSESLWEECTSCRGNGQTTRTCNNPSVOHGGRCBGNAVEIMCNIIRPCPVHGA 4647

Qy 121 SAWQWGTCTSCSCGKGTQTRARLCNNPPPAFGGSCYCDGAETQVQCNERNCPHGWATW 180
Db 4648 SAWQWGTCTSCSCGKGTQTRARLCNNPPPAFGGSCYCDGAETQVQCNERNCPHGWATW 4707

Qy 181 ASWSACSVSCGGARQTRCGSDPVPOY 208
Db 4708 ASWSACSVSCGGARQTRCGSDPVPOY 4735

RESULT 11
US-10-114-153-86
; Sequence 86, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glenda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernyev, Veilizar
; APPLICANT: Gangoli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spyttek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina

; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACID
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 86
; LENGTH: 2572
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-153-86

Query Match 99.9%; Score 1230; DB 14; Length 2572;
Best Local Similarity 99.5%; Pred. No. 9.4e-92;
Matches 207; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGFSQSAWRACSVTCGKGIQKSRCLNQLPANGKPKCGSDLEMRNCKPCPD 60
Db 1581 QVHGFSQSAWRACSVTCGKGIQKSRCLNQLPANGKPKCGSDLEMRNCKPCPD 1640

Qy 61 GSWSESLWEECTSCRGNGQTTRTCNNPSVOHGGRCBGNAVEIMCNIIRPCPVHGA 120
Db 1641 GSWSESLWEECTSCRGNGQTTRTCNNPSVOHGGRCBGNAVEIMCNIIRPCPVHGA 1700

Qy 121 SAWQWGTCTSCSCGKGTQTRARLCNNPPPAFGGSCYCDGAETQVQCNERNCPHGWATW 180
Db 1701 SAWQWGTCTSCSCGKGTQTRARLCNNPPPAFGGSCYCDGAETQVQCNERNCPHGWATW 1760

Qy 181 ASWSACSVSCGGARQTRCGSDPVPOY 208
Db 1761 ASWSACSVSCGGARQTRCGSDPVPOY 1788

RESULT 12
US-10-120-801-76
; Sequence 76, Application US/10120801
; Publication No. US20030203843A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spyttek, Kimberly
; APPLICANT: Metraban, Fuad
; APPLICANT: Topper, James N.
; APPLICANT: Malyankar, Uriel
; APPLICANT: Wasserman, Scott

```

APPLICANT: Edinger, Shlomit
APPLICANT: Smithson, Glennda
APPLICANT: Gunther, Erik
APPLICANT: Komuves, Laszlo
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-340
CURRENT APPLICATION NUMBER: US/10/120,801
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/285748
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 60/286068
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/286292
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/288334
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/291241
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/322284
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/285609
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 76
LENGTH: 2673
TYPE: PRT
ORGANISM: human
FEATURE:
NAME/KEY: VARIANT
LOCATION: (119)
OTHER INFORMATION: Wherein Xaa is any amino acid.

US-10-120-801-76

Query Match 99.9%; Score 1230; DB 14; Length 2673;
Best Local Similarity 99.5%; Pred. No. 9.7e-92; Indels 0; Gaps 0;
Matches 207; Conservative 1; Mismatches 0;
QY 1 QVHGFQSWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPKCGSDLEVRNCKPKCPVD 60
Db 1565 QVHGFQSWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPKCGSDLEVRNCKPKCPVD 1624
QY 61 GSWSESLWEETRSCGRGNQTRTRTCNNPVSVOHGGPCEGNAVEIIMCNIRPCPVHGA 120
Db 1625 GSWSESLWEETRSCGRGNQTRTRTCNNPVSVOHGGPCEGNAVEIIMCNIRPCPVHGA 1684
QY 121 SAWQPMGTCSGCKGTQTRARLCNNPPAFGGSYCDGAETQMVQCNERNCPHKGKWTW 180
Db 1685 SAWQPMGTCSGCKGTQTRARLCNNPPAFGGSYCDGAETQMVQCNERNCPHKGKWTW 1744
QY 181 ASWSACSVSCGGGARQTRGCDPVPQY 208
Db 1745 ASWSACSVSCGGGARQTRGCDPVPQY 1772

RESULT 13
US-10-032-189-127
Sequence 127, Application US/10032189
Publication No. US20030170630A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Shimkets, Richard A
APPLICANT: Grosee, William M
APPLICANT: Szekeres, Edward S
APPLICANT: Vernet, Corine A.M.

APPLICANT: Li, Li
APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc L
APPLICANT: Gorman, Linda
APPLICANT: Gangolli, Esha A
APPLICANT: Fernandes, Elma R
APPLICANT: Rieger, Daniel K
APPLICANT: Edinger, Shlomit R
APPLICANT: Gunther, Erik
APPLICANT: Millet, Isabelle
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/274,192
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/277,826
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/282,981
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/309,247
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/311,754
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 127
LENGTH: 3645
TYPE: PRT
ORGANISM: Homo sapiens
US-10-032-189-127
Query Match 99.9%; Score 1230; DB 14; Length 3645;
Best Local Similarity 99.5%; Pred. No. 1.3e-91;
Matches 207; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVHGFQSWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPKCGSDLEVRNCKPKCPVD 60
Db 2537 QVHGFQSWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPKCGSDLEVRNCKPKCPVD 2596
QY 61 GSWSESLWEETRSCGRGNQTRTRTCNNPVSVOHGGPCEGNAVEIIMCNIRPCPVHGA 120
Db 2597 GSWSESLWEETRSCGRGNQTRTRTCNNPVSVOHGGPCEGNAVEIIMCNIRPCPVHGA 2656
QY 121 SAWQPMGTCSGCKGTQTRARLCNNPPAFGGSYCDGAETQMVQCNERNCPHKGKWTW 180
Db 2657 SAWQPMGTCSGCKGTQTRARLCNNPPAFGGSYCDGAETQMVQCNERNCPHKGKWTW 2716
QY 181 ASWSACSVSCGGGARQTRGCDPVPQY 208
Db 2717 ASWSACSVSCGGGARQTRGCDPVPQY 2744

RESULT 14
US-10-138-588-20
Sequence 20, Application US/10138588
Publication No. US20040018594A1

; GENERAL INFORMATION:
 ; APPLICANT: Alsobrook et al.
 ; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACID
 ; FILE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
 ; FILE REFERENCE: 21402-347A
 ; CURRENT APPLICATION NUMBER: US/10/138,588
 ; CURRENT FILING DATE: 2002-05-01
 ; PRIOR APPLICATION NUMBER: 60/288,395
 ; PRIOR FILING DATE: 2001-05-03
 ; PRIOR APPLICATION NUMBER: 60/308,901
 ; PRIOR FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: 60/313,388
 ; PRIOR FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: 60/324,757
 ; PRIOR FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: 60/288,900
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 203
 ; SEQ ID NO 20
 ; LENGTH: 4495
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-138-588-20

Query Match 99.9%; Score 1230; DB 15; Length 4495;
 Best Local Similarity 99.5%; Pred. No. 1.6e-91;
 Matches 207; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVHGFSQSAWRACSVTCGKIQKSRSLCNQPLPANGKPKCGSDLEVRNCONKPCPYD 60
 DB 3387 QVHGFSQSAWRACSVTCGKIQKSRSLCNQPLPANGKPKCGSDLEVRNCONKPCPYD 3446
 QY 61 GSWSESLWEECTRCGRGNQTRTCNNPVSQHGGRPCEGNAVEIIMCNIRPCPVHGW 120
 DB 3447 GSWSESLWEECTRCGRGNQTRTCNNPVSQHGGRPCEGNAVEIIMCNIRPCPVHGW 3506
 QY 121 SAWPMGTCSGKGTQTRARLCNNPPAPFGSSYCDGAETQMCNERNCPHKGKATW 180
 DB 3507 SAWPMGTCSGKGTQTRARLCNNPPAPFGSSYCDGAETQMCNERNCPHKGKATW 3566
 QY 181 ASWSACSVSCGGARQTRCGSDPVPQY 208
 DB 3567 ASWSACSVSCGGARQTRCGSDPVPQY 3594

RESULT 15
 US-10-019-065A-31
 ; Sequence 31, Application US/10019065A
 ; Publication No. US20040086501A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Corporation
 ; TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
 ; FILE REFERENCE: MSB-7265-PCT
 ; CURRENT APPLICATION NUMBER: US/10/019,065A
 ; CURRENT FILING DATE: 2002-08-30
 ; PRIOR APPLICATION NUMBER: US 60/266,300
 ; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 31
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-019-065A-31

Query Match 95.0%; Score 1169; DB 15; Length 197;
 Best Local Similarity 100.0%; Pred. No. 8.3e-88;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 QWSAWRACSVTCGKIQKSRSLCNQPLPANGKPKCGSDLEVRNCONKPCPYDVGSWSEWS 67
 DB 1 QWSAWRACSVTCGKIQKSRSLCNQPLPANGKPKCGSDLEVRNCONKPCPYDVGSWSEWS 60

QY 68 LWEECTRCGRGNQTRTCNNPVSQHGGRPCEGNAVEIIMCNIRPCPVHGWSAWQFWG 127
 DB 61 LWEECTRCGRGNQTRTCNNPVSQHGGRPCEGNAVEIIMCNIRPCPVHGWSAWQFWG 120
 QY 128 TCSESCGKGTQTRARLCNNPPAPFGSSYCDGAETQMCNERNCPHKGKATWASWACS 187
 DB 121 TCSESCGKGTQTRARLCNNPPAPFGSSYCDGAETQMCNERNCPHKGKATWASWACS 180
 QY 188 VSCGGARQTRCGSDP 204
 DB 181 VSCGGARQTRCGSDP 197

Search completed: November 17, 2004, 16:07:23
 Job time : 141 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2004, 15:44:52 ; Search time 40 Seconds
(without alignments)

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(without alignments)
500.327 Million cell updates/sec
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Title: US-10-019-065A-1

Perfect score: 1231
Sequence: 1 QVHGGSQSAWRACSVTCG.....SCGGARQRTGCSDPVPOY 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:★

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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	522.5	42.4	1074	2	JC5928	semaphorin F precursor
2	519.5	42.2	1584	2	T00026	brain-specific angiotensin
3	503.5	40.9	984	2	T00326	hypothetical protein
4	503.5	40.9	1522	2	T00028	brain-specific angiotensin
5	492.5	40.0	1170	2	A0558	thrombospondin 1 protein
6	489.5	39.8	1572	2	T00027	brain-specific angiotensin
7	488.5	39.7	1170	1	TSHUP1	thrombospondin 1 protein
8	474.5	38.5	437	2	S05478	proprotein convertase
9	472	38.3	1444	2	T18856	angiogenesis inhibitor
10	466	37.9	1178	1	A39804	thrombospondin 2 protein
11	453	36.8	1172	1	TSHUP2	thrombospondin 2 protein
12	451.5	36.7	1172	2	A45587	thrombospondin 2 protein
13	449	36.5	469	1	S29126	proprotein convertase
14	441	35.8	957	2	T15976	hypothetical protein
15	417.5	33.9	788	2	T25061	hypothetical protein
16	325.5	26.4	712	2	A45638	immunoglobulin-like
17	311	25.3	724	2	A48569	immunoglobulin-like
18	304.5	24.7	206	2	A48517	immunoglobulin-like
19	296.5	24.1	803	2	A47723	coccidioides-related
20	287.5	23.4	807	2	A38152	F-spondin - rat
21	276	22.4	2165	2	T21371	hypothetical protein
22	262	21.3	1360	2	T33922	hypothetical protein
23	257	20.9	805	2	T34212	hypothetical protein
24	257	20.9	860	2	T16892	hypothetical protein
25	242.5	19.7	951	2	T00260	hypothetical protein
26	237.5	19.3	254	2	T15952	hypothetical protein
27	235	19.1	919	2	T33541	unc-5 protein - Caenorhabditis
28	235	19.1	947	1	B43594	unc-5 protein, long isoform
29	231.5	18.8	1558	2	C89114	protein C37C3.6a

30	231.5	18.8	2167	2	T34395	hypothetical prote
31	221.5	18.0	951	2	T00017	gene ADAMTS-1 prot
32	220.5	17.9	898	2	T14764	hypothetical prote
33	219	17.8	1059	2	T22545	hypothetical prote
34	211.5	17.2	550	2	T47158	hypothetical prote
35	204.5	16.6	1205	2	T18517	procollagen N-endo
36	200	16.2	837	2	T00355	hypothetical prote
37	198.5	16.1	2098	2	T18397	protein CRP - mal
38	173.5	14.1	590	2	I46687	complement compone
39	164.5	13.4	152	2	D89753	protein FltC7.2 [i
40	164.5	13.4	654	2	T29247	hypothetical prote
41	155	12.6	334	2	T20524	hypothetical prote
42	153.5	12.5	591	1	C8HUB	complement C8 beta
43	146.5	11.9	934	1	A34372	complement C6 beta
44	145	11.8	843	1	A27340	complement C7 prec
45	144.5	11.7	293	2	T20523	hypothetical prote

ALIGNMENTS

RESULT 1

JC9328
 semaphorin F precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
 C:Accession: JC9328
 R:Simmons, A.D.; Prieschel, A.W.; McPherson, J.D.; Overhauser, J.; Lovett, M.
 Biochem. Biophys. Res. Commun. 242, 685-691, 1998
 A:Title: Molecular cloning and mapping of human semaphorin F from the Cri-du-chat candid
 A:Reference number: JC9328; MUID:98125554; PMID:946478
 A:Accession: JC9328
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1074 <SIM>
 A:Cross-references: UNIPROT:Q13591; GB:U52840; NID:G2772583; PIDN:AAC09473.1; PID:G27725
 A:Experimental source: brain
 C:Comment: This protein disrupts normal brain development and leads to some of the featu
 C:Genetics:
 A:Gene: semaf
 C:Superfamily: human semaphorin F; thrombospondin type 1 repeat homology
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:50-533/Domain: semaphorin #status predicted <SEM>
 F:840-896/Domain: thrombospondin type 1 repeat homology <THR3>
 F:971-993/Domain: transmembrane #status predicted <TMW>

Query Match	42.4%;	Score 522.5;	DB 2;	Length 1074;
Best Local Similarity	33.1%;	Pred. No. 1e-31;		
Matches 95: Conservative	24;	Mismatches 81;	Indels 87;	Gaps 3;

[illegible]

RESULT 2
T00026

brain-specific angiogenesis inhibitor 1 - human
 N:Alternate names: BAI1 protein
 C:Species: Homo sapiens (man)
 C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
 C/Accession: T00026
 R:Nishimori, H.; Shiratsuchi, T.; Urano, T.; Kimura, Y.; Kiyono, K.; Tatsumi, K.; Yoshida
 submitted to the EMBL Data Library, June 1997
 A:Reference number: 214064
 A/Accession: T00026
 A/Status: translated from GB/EMBL/DBDJ
 A/Molecule type: mRNA
 A/Residues: 1-1584 <NIS>
 A/Cross-references: UNIPROT:O14514; EMBL:AB005297; NID:d1175078; PID:d1024528
 A/Experimental source: brain
 C/Genetics:
 A/Gene: GDB:BAI1
 A/Cross-references: GDB:9838088; OMIM:602682
 A/Map position: 8q24-8q24
 F:408-462/Domain: thrombospondin type 1 repeat homology <THR3>
 Query Match 42.2%; Score 519.5; DB 2; Length 1584;
 Best Local Similarity 45.8%; Pred. No. 2.3e-31;
 Matches 92; Conservative 25; Mismatches 73; Indels 11; Gaps 5;
 QY 8 QWSAWRACSVTCGKGIQKRSLCNQPLPANGKPCQGSQSDLEMRNCQKP-CPVDGWSW 66
 DB 359 EWSFWSVCSSTCGEGWQTRTRFC--VSSSVSTQCSGPLREQLCNNSAVCPVHGAWDEW 415
 QY 67 SLNEECTRS CGRGNQTRTCNNPNSVQHGGRPCGNAVEIIMCNIRPCP---VHGAWSAW 123
 DB 416 SPWLSLSTCGRGRDRTRCRPP--QFGNGPCGPKQKFNALCPGRVADGNW 473
 QY 124 QPWGTCSESCGKGTQTRARLCNNPPAFGSGYCDGAEQTMQVNCNRPCHGKWATWASW 183
 DB 474 SSWACASCSQGRQRTRECN--PSYGAECQGHVETRDCLQCPVDGKQWQWASW 531
 QY 184 SACSVCSCGGARQRTGCSDP 204
 DB 532 GSCSVTCGAGSQRREVCSPG 552
 RESULT 3
 T00326
 hypochromal protein KIAA0550 - human
 C:Species: Homo sapiens (man)
 C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 15-Mar-2004
 C/Accession: T00326
 R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
 DNA Res. 5, 31-39, 1998
 A>Title: Prediction of the coding sequences of unidentified human genes. IX. The completed
 A/Reference number: 214086; MUID:98290545; PMID:9628581
 A/Accession: T00326
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-984 <NAG>
 A/Cross-references: EMBL:AB011122; NID:g3043623; PIDN:BA225476.1; PID:g3043624
 A/Experimental source: brain
 C/Genetics:
 A/Note: KIAA0550
 F:344-398/Domain: thrombospondin type 1 repeat homology <THR3>
 Query Match 40.9%; Score 503.5; DB 2; Length 984;
 Best Local Similarity 46.0%; Pred. No. 2.4e-30;
 Matches 93; Conservative 15; Mismatches 85; Indels 9; Gaps 4;
 QY 5 GFSQSWARACSVTCGKGIQKRSLCNQPLPANGKPCQGSQSDLEMRNCQKP-CPVDGWSW 63
 DB 293 GVEEWSQWSTCSVTGCGSQVTRTCVSPY---GTHCSGPLRESRVNNTALCPVHG 348
 QY 64 SEWSLWEECTRS CGRGNQTRTCNNPNSVQHGGRPCGNAVEIIMCNIRPCPVGAWSAW 123
 DB 349 EWSFWSLCSFTCGRGRQTRTRCTPP--QYGRPCGPEPTHKPCNIALCPVDGQWQW 406
 QY 124 QPWGTCSESCGKGTQTRARLCNNPPAFGSGYCDGAEQTMQVNCNRPCHGKWATWASW 183
 DB 407 SSWSCSVTCNGTQQRRCQT--AAHGGSECRGPWAESRECYNPECTANGQWQWGH 464
 QY 184 SACSVCSCGGARQRTGCSDPV 205
 DB 465 SGCSKSCDGGWERRIRTCQGA 486
 RESULT 5
 A40558
 thrombospondin 1 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C/Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
 C/Accession: A40558; A37305; B42587; 568787
 R:Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
 Genomics 11, 587-600, 1991
 A>Title: Characterization of the murine thrombospondin gene.
 A/Reference number: A40558; MUID:92128941; PMID:1774063
 A/Accession: A40558
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1170 <LAW>
 A/Cross-references: UNIPROT:P35441; GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M62453;
 ; GB:M62464; GB:M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:G51186
 R:Bornstein, P.; Alf, D.; Devarayalu, S.; Framson, P.; Li, P.
 J. Biol. Chem. 265, 16691-16698, 1990
 A>Title: Characterization of the mouse thrombospondin gene and evaluation of the role of
 A/Reference number: A37305; MUID:90375546; PMID:2398070

QY 124 QPWGTCSESCGKGTQTRARLCNNPPAFGSGYCDGAEQTMQVNCNRPCHGKWATWASW 183
 DB 407 SSWSCSVTCNGTQQRRCQT--AAHGGSECRGPWAESRECYNPECTANGQWQWGH 464
 QY 184 SACSVCSCGGARQRTGCSDPV 205
 DB 465 SGCSKSCDGGWERRIRTCQGA 486
 RESULT 4
 T00028
 brain-specific angiogenesis inhibitor 3 - human
 N:Alternate names: BAI3 protein
 C:Species: Homo sapiens (man)
 C/Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
 C/Accession: T00028
 R:Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.
 Cytogenet. Cell Genet. 79, 103-108, 1997
 A>Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-s
 A/Reference number: 214066; MUID:98194217; PMID:9533023
 A/Accession: T00028
 A/Status: translated from GB/EMBL/DBDJ
 A/Molecule type: mRNA
 A/Residues: 1-1522 <SHI>
 A/Cross-references: UNIPROT:O60242; EMBL:AB005299; NID:g3021700; PIDN:BA225363.1; PID:g30
 A/Experimental source: brain
 C/Genetics:
 A/Gene: GDB:BAI3
 A/Cross-references: GDB:9838090; OMIM:602684
 A/Map position: 6q12-6q12
 F:344-398/Domain: thrombospondin type 1 repeat homology <THR3>
 Query Match 40.9%; Score 503.5; DB 2; Length 1522;
 Best Local Similarity 46.0%; Pred. No. 3.5e-30;
 Matches 93; Conservative 15; Mismatches 85; Indels 9; Gaps 4;
 QY 5 GFSQSWARACSVTCGKGIQKRSLCNQPLPANGKPCQGSQSDLEMRNCQKP-CPVDGWSW 63
 DB 293 GVEEWSQWSTCSVTGCGSQVTRTCVSPY---GTHCSGPLRESRVNNTALCPVHG 348
 QY 64 SEWSLWEECTRS CGRGNQTRTCNNPNSVQHGGRPCGNAVEIIMCNIRPCPVGAWSAW 123
 DB 349 EWSFWSLCSFTCGRGRQTRTRCTPP--QYGRPCGPEPTHKPCNIALCPVDGQWQW 406
 QY 124 QPWGTCSESCGKGTQTRARLCNNPPAFGSGYCDGAEQTMQVNCNRPCHGKWATWASW 183
 DB 407 SSWSCSVTCNGTQQRRCQT--AAHGGSECRGPWAESRECYNPECTANGQWQWGH 464
 QY 184 SACSVCSCGGARQRTGCSDPV 205
 DB 465 SGCSKSCDGGWERRIRTCQGA 486
 RESULT 5
 A40558
 thrombospondin 1 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C/Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
 C/Accession: A40558; A37305; B42587; 568787
 R:Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
 Genomics 11, 587-600, 1991
 A>Title: Characterization of the murine thrombospondin gene.
 A/Reference number: A40558; MUID:92128941; PMID:1774063
 A/Accession: A40558
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1170 <LAW>
 A/Cross-references: UNIPROT:P35441; GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M62453;
 ; GB:M62464; GB:M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:G51186
 R:Bornstein, P.; Alf, D.; Devarayalu, S.; Framson, P.; Li, P.
 J. Biol. Chem. 265, 16691-16698, 1990
 A>Title: Characterization of the mouse thrombospondin gene and evaluation of the role of
 A/Reference number: A37305; MUID:90375546; PMID:2398070

A:Accession: A37905
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-490 <BOR>
A:Cross-references: GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40431.1; PID:g554390
R:Laberty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A:Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A:Reference number: A42587; MUID:92147683; PMID:1371115
A:Accession: B42587
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1152, 'P', 1154-1170 <LAH>
A:Cross-references: GB:M87276
A:Note: sequence extracted from NCBI backbone (NCBIP:81501)
R:Chen, H.; Aeschlimann, D.; Nowien, J.; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
A:Title: Expression and initial characterization of recombinant mouse thrombospondin 1
A:Reference number: S68787; MUID:96234006; PMID:8654563
A:Accession: S68787
A:Molecule type: protein
A:Residues: 19-26, 'X', 28-37 <CHE>
C:Complex: homotrimer, disulfide linked
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von
Willebrand factor type 1 repeat homology
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-1170/Product: thrombospondin 1 #status predicted <MAT>
F:317-375/Domain: von Willebrand factor type C repeat homology <VWC>
F:378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F:434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F:491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F:551-586/Domain: EGF homology <EGF>
F:248,360,708,1067/Binding site: carbohydrate (Asn) #status predicted
Query Match 40.0%; Score 492.5; DB 2; Length 1170;
Best Local Similarity 42.8%; Pred. No. 1.9e-29;
Matches 93; Conservative 23; Mismatches 74; Indels 27; Gaps 6;
QY 5 GFQSWAWRACSVTCGKGIQKRSRLCNQPLPANGKPGCGQSDLEMRNCKPKC---PVD 60
DB 381 GWSPSEWNTSCATCGNGIQGRSCD----SLNRCBGSVQTRTCHIQCDKRFQD 435
QY 61 GSWSEVSLMBEETRSCGRGNQTRTCNNPSPVHGGRPCGNAVEIIMCNIIRPCPVHGAWSAQPW 120
DB 436 GWSHSPSSSCSVTCGDGVTIRLCNPSFPQMGKPCGEARETKACKDACPINGGW 495
QY 121 SAMQPGTCSGSGKGTQTRARLCNNPPPAFGSGYCDGAEATQMVQNCERNCPHGG---- 175
DB 496 GPNSPWDICSVTCGGVQRSLRCNNPTFQFGKQCVGVTENQVNCNKQDCPDIDGLSNP 555
QY 176 -----KWATW--SACSVCGGGARQRTRGCS 203
DB 556 CFAGAKCTSPDGSKGACGACPGYSGNGIQ----CKD 588
RESULT 6
T00027
Brain-specific angiogenesis inhibitor 2 - human
N:Alternate names: BAI2 protein
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00027
R:Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.
Cytogenet. Cell Genet. 79, 103-108, 1997
A:Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-
A:Reference number: Z14066; MUID:98194217; PMID:9533023
A:Accession: T00027
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1572 <SHI>
A:Cross-references: UNIPROT:O60241; EMBL:AB005298; NID:g3021698; PIDN:BA25362.1; PID:g3
A:Experimental source: brain
C:Genetics:

A:Gene: GDB:BAI2
A:Cross-references: GDB:9838089; OMIM:602683
A:Map position: lp35-lp35
Query Match 39.8%; Score 489.5; DB 2; Length 1572;
Best Local Similarity 44.9%; Pred. No. 3.9e-29;
Matches 88; Conservative 27; Mismatches 72; Indels 9; Gaps 5;
QY 8 QWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPGCGQSDLEMRNCKPKC---PVDGSGWSEW 66
DB 302 EWSPMVSVCLTCGQGLQVTRTSC---VSSPYGTLCGFLRETRPCNNSATCPVHGVMEW 358
QY 67 SLWEECTRSCGRGNQTRTCNNPSPVHGGRPCGNAVEIIMCNIIRPCPVHGAWSAQPW 126
DB 359 GSWSLCSRSRSGRGRSRNRTCVPP--GAGKACGEGPLQTKLCSMAACPFEGQWLEHGPW 416
QY 127 GTCSECGKGTQTRARLCNNPPPAFGSGYCDGAEATQMVQNCERNCP--IHGKWATWASWSA 185
DB 417 GPCSTSCANGTQQRSRKCSVAGPAW--ATCTGALTDTRECSNLECPATDSKGGPWNWSL 474
QY 186 CSVSCGGGARQRTRG 201
DB 475 CSKTCDTGWQRRFRMC 490
RESULT 7
TSHUP1
Thrombospondin 1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 23-Aug-1987 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: A26155; A34274; A30140; A25812; A05172; A42927
R:Lawler, J.; Hynes, R.O.
J. Cell Biol. 103, 1635-1648, 1986
A:Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple c
A:Reference number: A26155; MUID:87057617; PMID:2430973
A:Accession: A26155
A:Molecule type: mRNA
A:Residues: 1-1170 <LAH>
A:Cross-references: UNIPROT:P07996; GB:X04665; NID:g37137; PIDN:CAA28370.1; PID:g37138
A:Note: parts of this sequence, including the amino end of the mature protein, were deter
R:Laberty, C.D.; Gierman, T.M.; Dixit, V.M.
J. Biol. Chem. 264, 11222-11227, 1989
A:Title: Characterization of the promoter region of the human thrombospondin gene. DNA s
A:Reference number: A34274; MUID:89291870; PMID:2544587
A:Accession: A34274
A:Molecule type: DNA
A:Residues: 1-166 <LAH>
A:Cross-references: GB:J04835
R:Hennessey, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, J.
J. Cell Biol. 108, 729-736, 1989
A:Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the
A:Reference number: A30140; MUID:89139590; PMID:2918029
A:Accession: A30140
A:Molecule type: mRNA
A:Residues: 1-83, 'A', 85-522, 'A', 524-1170 <HEN>
A:Cross-references: EMBL:X14787; NID:g37464; PIDN:CAA32889.1; PID:g37465
A:Note: parts of this sequence, including the amino end of the mature protein, were dete
R:Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A:Title: Partial amino acid sequence of human thrombospondin as determined by analysis o
A:Reference number: A25812; MUID:87157592; PMID:3030396
A:Accession: A25812
A:Molecule type: mRNA
A:Residues: 1-83, 'A', 85-397 <KOB>
A:Cross-references: GB:M25631; NID:g538353; PIDN:AAA36741.1; PID:g538354
R:Dixit, V.M.; Hennessey, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
A:Reference number: A05172; MUID:86287276; PMID:3461443
A:Accession: A05172
A:Molecule type: mRNA
A:Residues: 1-83, 'A', 85-374, 'RC' <DIX>
A:Cross-references: GB:M14326; NID:g340005; PIDN:AAA61237.1; PID:g553801
A:Note: parts of this sequence, including the amino end of the mature protein, were dete

R;Sun, X.; Skorstengaard, K.; Mosher, D.F.
J. Cell Biol. 118, 693-701, 1992
A:Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A:Reference number: A42927; MUID: 92348511; PMID: 1379247
A:Accession: A42927
A:Molecule type: protein
A:Residues: 987-1003 <SUN>
A:Note: Cys-992 is shown to have a free sulphydryl
C:Genetics:
A:Gene: GDB:THS1; TSP1; TSP
A:Cross-references: GDB:120438; OMIM:188060
A:Map position: 15q15-15q15
A:Introns: 23/1
A:Note: the list of introns may be incomplete
C:Complex: homotrimer, disulfide linked
C:Function:
A:Description: participates in cell migration and adhesion, and in platelet aggregation
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von
C:Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-1170/Product: thrombospondin 1 #status predicted <MAT>
F:317-375/Domain: von Willebrand factor type C repeat homology <WVC>
F:378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F:434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F:491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F:551-586/Domain: EGF homology <EGF1>
F:650-689/Domain: EGF homology <EGF2>
F:926-928/Region: cell attachment (R-G-D) motif
F:171-232/disulfide bonds: #status predicted
F:248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:270,274/disulfide bonds: interchain #status predicted
F:610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:1051/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 39.7%; Score 488.5; DB 1; Length 1170;
Best Local Similarity 41.9%; Pred. No. 3.7e-29;
Matches 91; Conservative 26; Mismatches 73; Indels 27; Gaps 6;

QY 5 GFSQSWAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSLEMRNCQKPC---PVD 60
Db 381 GWSFMSWSTSCSTCGNGIQQRGSCD-----SLNRCGSSVQTRCHIQECDKRFKQD 435

QY 61 GSWSESLWBEETRSCGRGNQTRTCNNPNSVQHGGPCGNAVEIMCNIRPCPVHGAW 120
Db 436 GGSWHSFMSWSTSCSTCGNGIQQRGSCD-----SLNRCGSSVQTRCHIQECDKRFKQD 495

QY 121 SAWOPWGTCTSCSCGKGTQTRALCNPPAFGGSYCDGAEQVQVNERNCPIHG----- 175
Db 496 GWSFMSWSTSCSTCGNGIQQRGSCD-----SLNRCGSSVQTRCHIQECDKRFKQD 555

QY 176 -----KWATW--ASW--SACSVSCGGGARQTRGCSGD 203
Db 556 CFAGVKTCTYPDGSWKGACGPPGYSNGNGIQ-----CTD 588

RESULT 8
S05478
properdin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S05478
R:Goudis, D.; Reid, K.B.M.
Nature 335, 82-85, 1988
A:Title: Properdin, the terminal complement components, thrombospondin and the circumpo
A:Reference number: S05478; MUID: 88318954; PMID: 3045564
A:Accession: S05478
A:Molecule type: mRNA
A:Residues: 1-437 <GOU>
A:Cross-references: UNIPROT:P11680; EMBL:X12905; NID:q53786; PIDN:CAA31389.1; PID:q53787
C:Complex: a mixture of homodimers, homotrimers and homotetramers
C:Function:
A:Description: protects C3 convertase (C3bb) from rapid inactivation
A:Pathway: complement alternate pathway

C:Superfamily: human properdin precursor; thrombospondin type 1 repeat homology
C:Keywords: complement alternate pathway; glycoprotein; homodimer; homotetramer; homotrin
F:45-97/Domain: thrombospondin type 1 repeat homology <THR1>
F:104-160/Domain: thrombospondin type 1 repeat homology <THR2>
F:161-224/Domain: thrombospondin type 1 repeat homology <THR3>
F:225-282/Domain: thrombospondin type 1 repeat homology <THR4>
F:283-345/Domain: thrombospondin type 1 repeat homology <THR5>
F:346-408/Domain: thrombospondin type 1 repeat homology <THR6>
F:52,55,108,111,114,165,168,229,232,290,293,350,353,356/Modified site: 2'-mannosyl-trypt
F:366,396/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.5%; Score 474.5; DB 2; Length 437;
Best Local Similarity 40.7%; Pred. No. 1.9e-28;
Matches 88; Conservative 30; Mismatches 81; Indels 17; Gaps 8;

QY 4 GGSFQSWAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSLEMRNCQ-NKPCPVDS 62
Db 106 GGSFQSWAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSLEMRNCQ-NKPCPVDS 164

QY 63 WSESLWBEETRSCGRGNQ-----TRTRTCNNPNSVQH--GGRPCGNAVEIMCN-IRPCP 115
Db 165 WASNGPMSFSSGSLGGAQEPKTRSRSCSAPAFSHQPPGKPCSPGPAVEHKACSGLPCCP 224

QY 116 VHGSAWQWGTCTSCSCGKGTQTRALCNPPAFGGSYCDGAEQVQVNER-NCPIH 174
Db 225 VAGGWPMSFSSGSLGGAQEPKTRSRSCSAPAFSHQPPGKPCSPGPAVEHKACSGLPCCP 284

QY 175 GKWATWASWSAC-----SVSCGG--GARQTRGCSGD 203
Db 285 GEWEANGWSDCSRLMSINCEGTPGQGSRSRSCGD 320

RESULT 9
T18856
angiogenesis inhibitor homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18856; T24653
R:McMurray, A.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z19031
A:Accession: T18856
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1444 <WTL>
A:Cross-references: UNIPROT:Q8MYA8; EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:CO:
A:Experimental source: clone C02B4
R:McMurray, A.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z19917
A:Accession: T24653
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1444 <WT2>
A:Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:CO2B4.1
A:Experimental source: clone T07C5
C:Genetics:
A:Gene: CESP:CO2B4.1
A:Map position: X
A:Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 566/

Query Match 38.3%; Score 472; DB 2; Length 1444;
Best Local Similarity 41.7%; Pred. No. 7.4e-28;
Matches 88; Conservative 25; Mismatches 86; Indels 12; Gaps 7;

QY 4 GGSFQSWAWRACSVTCG-KGQKRSRLCNQPLPANGKPCQGSLEMRNCQ-NKPC---P 58
Db 1187 GGSFQSWAWRACSVTCG-KGQKRSRLCNQPLPANGKPCQGSLEMRNCQ-NKPC---P 1246

QY 59 VDGWSESLWBEETRSCGRGNQTRTCNNPNSVQHGGPCGNAVEIMCNIRPCPVH- 117
Db 1247 VDGWTDIAWSECTDYCRNGHRSRTFCANPKPSQGAQCTGSDFFELNPC-FDPARCHL 1305

```
QY 118 --GAWSAWPMGTCSGCKGTOTRARNLNNPPPAFGSGYCDGAETOMQVNCNRNC--PI 173
DB 1306 RDGWSWTSDWTTPCASGCGFGVQTRDRSCSSEPK-GGSCSGLAHQISLCLDLPACDHES 1364

QY 174 HOKWATWASACSVSVCGGARQRTGGSDP 204
DB 1365 DGEWSAWEWSGCMGNCGIGTRTRACVSP 1395

RESULT 10
A39804
thrombospondin precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A39804
R:Lawler, J.; Duquette, M.; Ferro, P.
J. Biol. Chem. 266, 8039-8043, 1991
A:Title: Cloning and sequencing of chicken thrombospondin.
A:Reference number: A39804; MUID:91217026; PMID:2022631
A:Accession: A39804
A:Molecule type: mRNA
A:Residues: 1-1178 <LAW>
A:Cross-references: UNIPROT:P35440; GB:M60853; NID:G212763; PIDN:AAA51437.1; PID:G212764
C:Superfamily: Chrombospondin I; EGF homology; thrombospondin type 1 repeat homology; von
F:325-383/Domain: von Willebrand factor type C repeat homology <VWC>
F:386-437/Domain: thrombospondin type 1 repeat homology <THR1>
F:442-498/Domain: thrombospondin type 1 repeat homology <THR2>
F:499-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:658-697/Domain: EGF homology <EGF>

Query Match 37.9%; Score 466; DB 1; Length 1178;
Best Local Similarity 43.9%; Pred. No. 1.8e-27;
Matches 87; Conservative 19; Mismatches 76; Indels 16; Gaps 3;

QY 5 GFSQSAWRACSVTCGKGIKESRLCNQPLPANGKPCQGSLEMRNCKPKCPV---VD 60
DB 389 GWSFSDWTCKSVTCGSGTQMRGSCDVTRSA-----CTGPHIQTRMCSFKKCDHRIRQD 443

QY 61 GSWSESLWEECTRCGRNQTRTRTCNNPVSQHGRCPCGNAVEIIMCNRPCPVHGW 120
DB 444 GWSHSPWSSCSVTCGVGNITRILCNSPIQMGKCKVGNRETKCEKAPCPVNGQW 503

QY 121 SAWQPMGTCSGCKGTOTRARNLNNPPPAFGSGYCDGAETOMQVNCNRNCPIHG----- 175
DB 504 GWSFMSACTVTCGGGIRERSRLCNSPEPYGKPCVGTQKQDMCKNRKDCPIDGCLSNP 563

QY 176 --KWATWASWASCSVSCG 191
DB 564 CFPGAECNSYPDGWSWCG 581

RESULT 11
TSHUP2
thrombospondin 2 precursor - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: A47379; A42173
R:LaBell, T.L.; Byers, P.H.
Genomics 17, 225-229, 1993
A:Title: Sequence and characterization of the complete human thrombospondin 2 cDNA: pote
A:Reference number: A47379; MUID:94010892; PMID:8406456
A:Accession: A47379
A:Molecule type: mRNA
A:Residues: 1-1172 <LAB>
A:Cross-references: UNIPROT:P35442; GB:U12350; NID:G307505; PIDN:AAA03703.1; PID:G307506
R:LaBell, T.L.; Milewicz, D.J.; Distche, C.M.; Byers, P.H.
Genomics 12, 421-429, 1992
A:Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression o
A:Reference number: A42173; MUID:92217961; PMID:1559694
A:Accession: A42173
A:Molecule type: mRNA
A:Residues: 560-1172 <LA2>
```

```
A:Cross-references: GB:M81339
A:Experimental source: fibroblast
A:Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBI:95096)
C:Genetics:
A:Gene: GDB:THBS2; TSP2
A:Cross-references: GDB:128789; OMIM:188061
A:Map position: 6q27-6q27
C:Complex: homotrimer, disulfide linked
C:Function:
A:Description: Participates in cell migration and adhesion, and in platelet aggregation
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von
C:Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-1172/Product: thrombospondin 2 #status predicted <MAT>
F:319-377/Domain: von Willebrand factor type C repeat homology <VWC>
F:380-431/Domain: thrombospondin type 1 repeat homology <THR1>
F:436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F:493-549/Domain: thrombospondin type 1 repeat homology <THR3>
F:553-588/Domain: EGF homology <EGF1>
F:652-691/Domain: EGF homology <EGF>
F:928-930/Region: cell attachment (R-G-D) motif
F:151,316,330,457,584,710,1069/Binding site: carbohydrate (Asn) (covalent) #status predic
F:167-226/Disulfide bonds: #status predicted
F:266-270/Disulfide bonds: interchain #status predicted
F:612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 36.8%; Score 453; DB 1; Length 1172;
Best Local Similarity 40.4%; Pred. No. 1.6e-26;
Matches 80; Conservative 26; Mismatches 76; Indels 16; Gaps 3;

QY 5 GFSQSAWRACSVTCGKGIKESRLCNQPLPANGKPCQGSLEMRNCKPKCPV---D 60
DB 383 GWSFMSACTVTCGSGTQMRGSCDVTRSA-----SNTCLGPSICTRACSLKCDTRIQD 437

QY 61 GSWSESLWEECTRCGRNQTRTRTCNNPVSQHGRCPCGNAVEIIMCNRPCPVHGW 120
DB 438 GWSHSPWSSCSVTCGVGNITRILCNSPVQMGKCKVGNRETKCAQCAPCPIDGRW 497

QY 121 SAWQPMGTCSGCKGTOTRARNLNNPPPAFGSGYCDGAETOMQVNCNRNCPIHG----- 175
DB 498 SPMSFMSACTVTCAGGIRERTVCSNPEPYGKPCVGTQKQDMCKNRKSCPDVDCGLSNP 557

QY 176 --KWATWASWASCSVSCG 191
DB 558 CFPGAECNSYPDGWSWCG 575

RESULT 12
A42587
thrombospondin 2 precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42587; A39851
R:LaHerty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A:Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A:Reference number: A42587; MUID:92147683; PMID:1371115
A:Accession: A42587
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-1172 <LAH>
A:Cross-references: UNIPROT:Q03350; GB:L07803; GB:M87275; NID:G340421; PIDN:AAA53064.1;
A:Note: sequence extracted from NCBI backbone (NCBI:81502)
R:Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.
J. Biol. Chem. 266, 12821-12824, 1991
A:Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.
A:Reference number: A39851; MUID:91302287; PMID:1712771
A:Accession: A39851
A:Molecule type: mRNA
A:Residues: 1-873 <BOR>
A:Cross-references: GB:M64866; NID:G201994; PIDN:AAA40432.1; PID:G201995
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vo
```

Residues: 1-60, 'X', 62-413, 'D', 415-452, 'XX', 455-469 <WE2>

Query Match

A: Molec

Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3; 461/2; 498/3;

A; Introns:

A; Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3; 4

A; Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3;

A; Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3;

Matches	85;	Conservative	22;	Mismatches	80;	Indels	50;	Gaps	5;
QY	1	QVHGFSQSAWRACSVTCGKGIQKRSRLCNQP-----	LPANG	38					
Db	657	RVGNWSWTWENHCSVSGRGSQARYKCLSPHRTLAPDCGENKVTNELRITFFKARS	716						
QY	39	GKPC-----	QSDLEMRNCQKPCPVDGSWSWSLWBECTRSCGRGQTRRT	86					
Db	717	YIMCSVRCKIKRNTISEKNIEVRSNDGPNCAIGWGTWGWSTCSTSCGPGTLVRQT	776						
QY	87	CNNPSVQHGGRCPEGNAVEIIMCNIRPCPVHGAWSAQWPWGTCSES CGKGTQTRARLCNN	146						
Db	777	CNR-----	EFCDGSAHRRSCNVATCQNDGINSLNWNSDCSRVCGKGLRSRSC--	827					
QY	147	PPPAFGSYCDGAETQMVCNERNCPH--GKWATWASWSACSVSCGGGARQTRGC	201						
Db	828	-----	FGSGCMGASSEQQFCNEQACASSANDWGTWSGWSQCSVSCGAGVKRTRTC	879					

RESULT 15
T25061
hypothetical protein T21B6.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25061
R:Cottage, A.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19975
A:Accession: T25061
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-788 <WIL>
A:Cross-references: UNIPROT:Q22631; EMBL:Z68011; PIDN:CAA92014.1; GSPDB:GN00028; CESP:T21B6
A:Experimental source: clone T21B6
C:Genetics:
A:Gene: CESP:T21B6.3
A:Map position: X
A:Introns: 20/1; 47/1; 76/1; 152/1; 735/2; 754/2

Query Match	33.9%;	Score	417.5;	DB	2;	Length	788;
Best Local Similarity	39.0%;	Pred. No.	5.3e-24;				
Matches	78;	Conservative	20;	Mismatches	79;	Indels	23;
Gaps	6;						
QY	2	VHGGFSQSAWRACSVTCGKGIQKRSRLCNQPLPANGKPKCGSDLEMCNQKPCPVDG	61				
Db	454	VSGVHWDMSDSTCTCGDGAKSRRECST-----	NNCGADYETEPFNLGPCQ---	503			
QY	62	SWSEWSLWBECTRSCGRGQTRTRTCNNPVSQHGGRPCEGNAVEIIMCNIRPCPVHGAWS	121				
Db	504	TWSEWCWSTCSASCSGQGRTRFCH-----	LGTNRCEGKDYSESQCSAGPCP---	555			
QY	122	AWQPMGTCSGCGKGTQTRARLCNNPPAPFGGSYCDGAETQMVCNERNCPHGWATWA	181				
Db	556	QWEDWQCQSVTCGGVAVRQRTCLG--	GVFGDHLCOGPKTEQACDGGFCSL---	WSPWQ	610		
QY	182	SWSACSVSCGGGARQTRGC	201				
Db	611	EWSTGSCGSGMKRRQRVC	630				

Search completed: November 17, 2004, 15:56:20
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2004, 15:30:24 ; Search time 194 Seconds

(without alignments)
616.897 Million cell updates/sec

Title: US-10-019-065A-1

Perfect score: 1231

Sequence: 1 QVHGGSQSAWRACSVTCG.....SCGGGARQTRGCSPPVPQY 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1231	100.0	5636	2 Q96RW7	Q96RW7 homo sapien
2	1230	99.9	2673	2 Q96SC3	Q96SC3 homo sapien
3	533.5	43.3	1077	1 SM5A_MOUSE	Q62217 mus musculus
4	530.5	43.1	1582	1 Q8CGM0	Q8CGM0 mus musculus
5	528.5	42.9	1388	2 Q7QKD0	Q7QKD0 anopheles g
6	522.5	42.4	1074	1 SM5A_HUMAN	Q13591 homo sapien
7	519.5	42.2	1584	1 BAI1_HUMAN	Q14514 homo sapien
8	511.5	41.6	1093	1 SM5B_HUMAN	Q9p283 homo sapien
9	511.5	41.6	1151	2 Q6DD89	Q6dd89 homo sapien
10	507.5	41.2	478	2 Q8BVE5	Q8bve5 m mus muscu
11	507.5	41.2	632	2 Q6ZPQ8	Q6zpq8 mus musculus
12	507.5	41.2	632	2 BAC98172	Bac98172 mus muscu
13	507.5	41.2	1093	1 SM5B_MOUSE	Q60519 mus musculus
14	506.5	41.1	1088	2 Q6PCK8	Q6pck8 xenopus lae
15	506.5	41.1	1088	2 AAH59288	AAH59288 xenopus l
16	504.5	41.0	612	2 Q6ZQ96	Q6zq96 mus musculus
17	504.5	41.0	612	2 BAC97972	Bac97972 mus muscu
18	504.5	41.0	1522	1 BAI3_MOUSE	Q80zf8 mus musculus
19	503.5	40.9	1522	1 BAI3_HUMAN	Q60242 homo sapien
20	500.5	40.7	1427	2 Q6DCS2	Q6dcs2 xenopus lae
21	496.5	40.3	1549	2 Q6Pgn0	Q6pgn0 mus musculus
22	496.5	40.3	1549	2 AAH56926	AAH56926 mus muscu
23	492.5	40.0	1170	1 TSPI_BOVIN	Q28178 bos taurus
24	492.5	40.0	1170	1 TSPI_MOUSE	P35441 mus musculus
25	492.5	40.0	1171	2 Q80YQ1	Q80yq1 mus musculus
26	492.5	40.0	1171	2 Q8CGB2	Q8cgb2 mus musculus
27	492.5	40.0	1560	2 Q8CGM1	Q8cgm1 mus musculus
28	490	39.8	1092	2 Q6UY12	Q6uy12 homo sapien
29	490	39.8	1092	2 AAQ88491	AAq88491 homo sapi
30	489.5	39.8	1572	1 BAI2_HUMAN	Q60241 homo sapien
31	489.5	39.8	1573	2 Q8NGW8	Q8ngw8 homo sapien

ALIGNMENTS

RESULT 1

Q56RW7

ID Q96RW7 PRELIMINARY; PRT; 5636 AA.

AC Q96RW7; (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Hemocentin.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Trent J.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF156100; AAK68690.1; -.

DR HSSP; P07996; 1LSL.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0005021; F:vascular endothelial growth factor receptor. .; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR00152; Asx_hydroxyl_S.

DR InterPro; IPR000875; Cecropin.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR006605; G2F.

DR InterPro; IPR003030; Grow_fac_recept.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_C2.

DR InterPro; IPR000169; Pept_cys_acsite.

DR InterPro; IPR000884; TSF1.

DR InterPro; IPR009134; VEGFR.

DR InterPro; IPR002035; VWF_A.

DR Pfam; PF07645; EGF_CA_8.

DR Pfam; PF07474; G2F_1.

DR Pfam; PF00047; Ig_44.

DR Pfam; PF00090; TSP_1; 6.

Query Match 100.0%; Score 1231; DB 2; Length 5636;
 Best Local Similarity 100.0%; Pred. No. 3.2e-89;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVHGFSQMSAWRACSVTCGKGIQKRSRLCNQPLPANGGKPCQGSDEMRNCQKPCPVD 60
 4528 QVHGFSQMSAWRACSVTCGKGIQKRSRLCNQPLPANGGKPCQGSDEMRNCQKPCPVD 4587

QY 61 GSWSEWSLWECTSCGRGNQTRTTCNNPVSQHGGRPCGNAVEIIMCNRPCPVHGA 120
 4588 GSWSEWSLWECTSCGRGNQTRTTCNNPVSQHGGRPCGNAVEIIMCNRPCPVHGA 4647

QY 121 SAWOPWGTCTSCSCGKGTQTRARLNCNPPAPFGSGYCDGAETQVNCNRCPIHGKWATW 180
 4648 SAWOPWGTCTSCSCGKGTQTRARLNCNPPAPFGSGYCDGAETQVNCNRCPIHGKWATW 4707

QY 181 ASWSACSVSCGGARQTRGSDVPVQY 208
 4708 ASWSACSVSCGGARQTRGSDVPVQY 4735

RESULT 2

Q96SC3 ID Q96SC3 PRELIMINARY; PRT; 2673 AA.

AC O96SC3; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Fbulin-6 (Fragment).

GN Name=FIBL-6;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]
 SEQUENCE FROM N.A.

RP Tissue=Melanoma;
 RA Kistka G., Timpi R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ306906; C37630.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR000152; Asx hydroxyl S.
 DR InterPro; IPR000875; Cectopin.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR06605; G2F.
 DR InterPro; IPR009017; G2F like.
 DR InterPro; IPR009030; Grow fac recept.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig c2.
 DR InterPro; IPR009138; Neural_cell_adh.
 DR InterPro; IPR000884; TSPI.
 DR InterPro; IPR008085; TSP 1.
 DR Pfam; PF07645; EGF_CA; 8.
 DR Pfam; PF07474; G2F; 1.
 DR Pfam; PF00047; Ig; 17.
 DR Pfam; PF00090; TSP 1; 6.
 DR PRINTS; PR01838; NCAMFAMILY.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00179; EGF_CA; 7.
 DR SMART; SM00408; IGC2; 17.
 DR SMART; SM00209; TSPI; 6.
 DR PROSITE; PS00010; ASX_HYDROXYL; 5.
 DR PROSITE; PS00268; CECTOPIN; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS00026; EGF_3; 5.
 DR PROSITE; PS01187; EGF_CA; 8.
 DR PROSITE; PS00835; IG_LIKE; 17.
 DR PROSITE; PS00092; TSPI; 6.

KW EGF-like domain.
 FT NON_TER 1
 SQ SEQUENCE 2673 AA; 291017 MW; BEABC30B8340E272 CRC64;

Query Match 99.9%; Score 1230; DB 2; Length 2673;
 Best Local Similarity 99.5%; Pred. No. 1.9e-89;
 Matches 207; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVHGFSQMSAWRACSVTCGKGIQKRSRLCNQPLPANGGKPCQGSDEMRNCQKPCPVD 60
 1565 QVHGFSQMSAWRACSVTCGKGIQKRSRLCNQPLPANGGKPCQGSDEMRNCQKPCPVD 1624

QY 61 GSWSEWSLWECTSCGRGNQTRTTCNNPVSQHGGRPCGNAVEIIMCNRPCPVHGA 120
 1625 GSWSEWSLWECTSCGRGNQTRTTCNNPVSQHGGRPCGNAVEIIMCNRPCPVHGA 1684

QY 121 SAWOPWGTCTSCSCGKGTQTRARLNCNPPAPFGSGYCDGAETQVNCNRCPIHGKWATW 180
 1685 SAWOPWGTCTSCSCGKGTQTRARLNCNPPAPFGSGYCDGAETQVNCNRCPIHGKWATW 1744

QY 181 ASWSACSVSCGGARQTRGSDVPVQY 208
 1745 ASWSACSVSCGGARQTRGSDVPVQY 1772

RESULT 3

SM5A_MOUSE ID SM5A_MOUSE STANDARD; PRT; 1077 AA.

AC Q62217; 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Semaphorin 5A precursor (Semaphorin F) (Sema F).

GN Name=Sema5a; Synonyms=Semaf, Semf;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.

RP STRAIN=NMRI;
 RA MEDLINE=96414430; PubMed=8817451;
 RA Adams R.H., Betz H., Puschel A.W.;
 RT "A novel class of murine semaphorins with homology to thrombospondin
 is differentially expressed during early embryogenesis.";
 RL Mech. Dev. 57:33-45(1996).

CC -!- FUNCTION: May act as positive axonal guidance cues.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: In adult, detected in liver, brain, kidney,
 CC heart, lung and spleen.
 CC -!- DEVELOPMENTAL STAGE: Differentially expressed in embryonic and
 CC adult tissues. Its abundance decreases from E10 to birth.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 7 TSP type-1 domains.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; X97817; CAA66397.1; -;
 DR HSSP; P07996; ILSL.
 DR MGD; MGI:107556; Sema5a.
 DR GO; GO:0016021; C:integral to membrane; IDA.
 DR GO; GO:0008046; P:axon guidance; IMP.
 DR GO; GO:0007411; P:axon guidance; IMP.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.

[illegible]

```

RESULT 5
Q7QKD0
ID Q7QKD0 PRELIMINARY; PRT; 1388 AA.
AC Q7QKD0;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE AGCPI4698 (fragment).

```

```

GN Name=agCG49943; ORFNames=ENSANGG00000019365;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
OX NCBI_TaxID=180454;
RV [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
DR EMBL; AAAB01008799; EAA03790.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00047; Ig; 6.
DR Pfam; PF00090; TSP 1; 4.
DR PRINTS; PR01705; TSP1REPEAT.
DR PROSITE; PS50835; IG LIKE; 9.
DR PROSITE; PS50092; TSP1; 4.
FT NON-TER 1388 1388
SQ SEQUENCE 1388 AA; 153015 MW; 3A054C8EF1900324 CRC64;

Query Match 42.9%; Score 528.5; DB 2; Length 1388;
Best Local Similarity 42.2%; Pred. No. 8.6e-34;
Matches 89; Conservative 36; Mismatches 77; Indels 9; Gaps 3;

Qy 6 PSQSAWRAACSVTCGKGIQKRLC--NQPLPANGK-PCQSDLEVRMCNQKPCPVDS 62
Db 1072 WSPKGAWSPCSATCGSGTQFRSICLLVNGSPAHERFNCVGENVELKACELLPCPVNG 1131
Qy 63 WSESLWEETRSC-----GRGNQTRTCNNPSVQHGRPCGKNAVELIMCNIRPCV 116
Db 1132 WGEWTGNSCLSCVSEFSGVRSIRKSRACDPAPSLGKQCVGEAYEEPCHYCPI 1191
Qy 117 HGAWSAQWPGTCSESGKGTQTRALCNPPPAFGSGYCDGAEQMVQVNERNCPIHGK 176
Db 1192 DGGWTAWSGWTGCEPCGSLRMRSCSNPVRHGLGLCDGAESEVKACKVQECHVDG3 1251
Qy 177 WATWASACSVSCGGGARORTGCDSPVQ 207
Db 1252 WSEWRSPCNKSGGKIKRRRYCNPEK 1282

RESULT 6
SM5A_HUMAN
ID SM5A_HUMAN STANDARD; PRT; 1074 AA.
AC Q13591; O60408;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Semaphorin 5A precursor (Semaphorin F) (Sema F).
GN Name=SEMA5A; Synonyms=SEMAF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RV [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98125554; PubMed=9464278;
RA Simmons A.D.; Fuschel A.W.; McPherson J.D.; Overhauser J.; Lovett M.;
RT "Molecular cloning and mapping of human semaphorin F from the Cri-du-
RT chat candidate interval.";
RL Biochem. Biophys. Res. Commun. 242:685-691(1998).
RN [2]
RP SEQUENCE OF 1-494 FROM N.A.
RA Kalicki J.; Harmon G.;
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: May act as positive axonal guidance cues.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the semaphorin family.

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CC -!- SIMILARITY: Contains 1 Sema domain.
CC -!- SIMILARITY: Contains 7 TSP type-1 domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U52840; AAC09473.1; -.
DR EMBL; AC004615; AAC14668.1; -.
DR FIR; JCS928; JCS928.
DR HSSP; P07996; ILSL.
DR Genew; HGNC:10736; SEMA5A.
DR GO; GO:0007155; P:cell adhesion; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007393; P:neurogenesis; TAS.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP 1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF00090; TSP 1; 6.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR SMART; SM00209; TSP1; 6.
DR PROSITE; PS51004; SEMA; 1.
DR PROSITE; PS50092; TSP1; 6.
KW Developmental protein; Glycoprotein; Multigene family; Neurogenesis;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 22
FT CHAIN 23 1074
FT DOMAIN 23 968
FT TRANSMEM 969 989
FT DOMAIN 990 1074
FT DOMAIN 35 484
FT DOMAIN 540 593
FT DOMAIN 595 651
FT DOMAIN 653 702
FT DOMAIN 707 765
FT DOMAIN 784 839
FT DOMAIN 841 896
FT DOMAIN 897 944
FT CARBOHYD 142 142
FT CARBOHYD 168 168
FT CARBOHYD 227 227
FT CARBOHYD 277 277
FT CARBOHYD 323 323
FT CARBOHYD 367 367
FT CARBOHYD 437 437
FT CARBOHYD 536 536
FT CARBOHYD 591 591
FT CARBOHYD 717 717
FT CARBOHYD 933 933
FT CONFLICT 56 56
FT CONFLICT 149 149
FT CONFLICT 382 382
FT CONFLICT 494 494
SQ SEQUENCE 1074 AA; 120570 MW; EE3DB763CBE29407 CRC64;

Query Match 42.4%; Score 522.5; DB 1; Length 1074;
Best Local Similarity 33.1%; Pred. No. 2e-33;
Matches 95; Conservative 24; Mismatches 81; Indels 87; Gaps 3;

Qy 3 HGFPSQSAWRAACSVTCGKGIQKRLCNPQLPANGKPCQSDLEVRMC-NQKPCPVDS 61
Db 595 NGWTPWTWSGPCSTTCGIGFQVRQSCSNPTPRHGGRVCGVQGNREERYCNEHLLCPPHM 654

```

QY 62 SMSWSLWECTSCRGNOTRTTCNNPSVOHGRPCBEGNAVEIMCNIIRCP----- 115
Db 655 FWTGWFWRCTAQCQGGIQAARRICEN-----GPDACGCVVEYOSCNTNCPBLKXTT 708
QY 116 ----- 115
Db 709 PWTPTVFNISDNGDHYEQFRYTKCARLADPNLLEVGQRLEMYCSDGTSGCGSTDGL 768
QY 116 -----VHGANSANQPMWTCSCGKGTQTARLCNNPPAFGSGYCDGAET 161
Db 769 SGDFLAGRYSAHTVNGASANTSQCSRDGSRGIRNKRVCNNPEPKYGMPCIGPSSL 828
QY 162 OMQVCNERNCPHKGKATWASKSACSVSGGARORTGCSDPVPOY 208
Db 829 EYQECNTLPCVDGVWSCSPWTKSATCGGHYMRTRSCSNPAPAY 875
RESULT 7
BAIL_HUMAN
ID BAIL_HUMAN STANDARD; PRT; 1584 AA.
AC O145T4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Brain-specific angiogenesis inhibitor 1 precursor.
GN Name=BAIL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retal brain;
RX MEDLINE=98054121; PubMed=9393972;
RA Nishimori H. Shiratsuchi T., Umano T., Kimura Y., Kiyono K.,
RA Tatsumi K., Yoshida S., Ono M., Kuwano M., Nakamura Y., Tokino T.;
RT "A novel brain-specific p53-target gene, BAIL1, containing
thrombospondin type 1 repeats inhibits experimental angiogenesis.";
RL Oncogene 15:2145-2150(1997).
RN [2]
RP INTERACTION WITH BAP1.
RX MEDLINE=98321173; PubMed=9647739;
RA Shiratsuchi T., Futamura M., Oda K., Nishimori H., Nakamura Y.,
RA Tokino T.;
RT "Cloning and characterization of BAI-associated protein 1: a PDZ
domain-containing protein that interacts with BAIL1.";
RL Biochem. Biophys. Res. Commun. 247:597-604(1998).
CC -!- FUNCTION: Likely to be a potent inhibitor of angiogenesis in brain
and may play a significant role as a mediator of the p53 signal in
suppression of glioblastoma. May function in cell adhesion and
signal transduction in the brain.
CC -!- SUBUNIT: Interacts with BAP1 and PHYHIP.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Likely to be
concentrated at cell-cell adhesion sites.
CC -!- TISSUE SPECIFICITY: Specifically expressed in brain. Reduced or no
expression is observed in some glioblastoma cell lines and cancer
tissues.
CC -!- INDUCTION: By p53.
CC -!- DOMAIN: The TSP1 repeats inhibit in vivo angiogenesis in rat
cornea induced by BFGF.
CC -!- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.
CC -!- LN-TM7 subfamily.
CC -!- SIMILARITY: Contains 1 GPS domain.
CC -!- SIMILARITY: Contains 5 TSP type-1 domains.
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CC -----

EMBL; AB005297; BAA23647.1; -.
PIR; T00026; T00026.
HSSP; P07996; ILSL.
Genew; HGNC:943; BAIL1.
MIM; 602682; -.
GO; GO:0005687; C:integral to plasma membrane; TAS.
GO; GO:0005911; C:intercellular junction; TAS.
GO; GO:0005515; F:protein binding; TAS.
GO; GO:0007409; P:axogenesis; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
GO; GO:0007422; P:peripheral nervous system development; TAS.
GO; GO:0007155; P:signal transduction; TAS.
InterPro; IPR008077; Angio_inhib.
InterPro; IPR008032; GPCR_secretin.
InterPro; IPR001879; Hormn_receptor.
InterPro; IPR00203; PKD_cys_rich.
InterPro; IPR000884; TSP1.
InterPro; IPR008085; TSP_1.
Pfam; PF00002; 7tm_2; 1.
Pfam; PF01825; GPS; 1.
Pfam; PF02793; HRM; 1.
Pfam; PF00090; TSP_1; 5.
PRINTS; PR01694; BAIPRECURSOR.
PRINTS; PR00249; GPCRSECRETIN.
PRINTS; PR01705; TSP1REPEAT.
SMART; SM00303; GPS; 1.
SMART; SM00008; Hormr; 1.
SMART; SM00209; TSP1; 5.
PROSITE; PS0221; GPS; 1.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FALSE_NEG.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
PROSITE; PS0092; TSP1; 5.
Cell adhesion; G-protein coupled receptor; Glycoprotein; Repeat;
Signal; Transmembrane.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 1584 Brain-specific angiogenesis inhibitor 1.
FT DOMAIN 31 948 Extracellular (Potential).
FT TRANSMEM 949 969 1 (Potential).
FT DOMAIN 970 980 Cytoplasmic (Potential).
FT TRANSMEM 981 1001 2 (Potential).
FT DOMAIN 1002 1008 Extracellular (Potential).
FT TRANSMEM 1009 1029 3 (Potential).
FT DOMAIN 1030 1052 Cytoplasmic (Potential).
FT TRANSMEM 1053 1073 4 (Potential).
FT DOMAIN 1074 1093 Extracellular (Potential).
FT TRANSMEM 1094 1114 5 (Potential).
FT DOMAIN 1115 1136 Cytoplasmic (Potential).
FT TRANSMEM 1137 1157 6 (Potential).
FT DOMAIN 1158 1166 Extracellular (Potential).
FT TRANSMEM 1167 1187 7 (Potential).
FT DOMAIN 1188 1584 Cytoplasmic (Potential).
FT TRANSMEM 1585 1584 TSP type-1 1.
FT DOMAIN 354 407 TSP type-1 2.
FT TRANSMEM 409 462 TSP type-1 3.
FT DOMAIN 467 520 TSP type-1 4.
FT TRANSMEM 522 575 TSP type-1 5.
FT DOMAIN 881 938 GPS.
FT TRANSMEM 1411 1422 Poly-Pro.
FT DOMAIN 1425 1430 Poly-Pro.
FT SITE 231 233 Cell attachment site (Potential).
FT DOMAIN 1365 1584 Necessary for interaction with BAP1.
FT TRANSMEM 1581 1584 Indispensable for interaction with BAP1.
FT TRANSMEM 64 64 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 401 401 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 607 607 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 692 692 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 844 844 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 877 877 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 881 881 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1584 AA; 173531 MW; DEAF28C77874513 CRC64;

QY 3 HGGFSONAWRACSVTCGKIQKSRCLNCPPLPANGKPCQGSLEMRNC-QNKPCPDVG 61
 Db 13 NGAWTANSSWAQCTSCGIGFQVRQSCSNPAPRHGGRICVGRSRERFCNENTPCFVPI 72
 QY 62 SWEWSLWEECTRCGRGNQTRTCTNNPSVQHGGRPCGNAVEIIMCNRPCP----- 115
 Db 73 FWASWGSWSKSCNNCGGVQSRSSCEN-----GNSCPGCGVEFKTCNPEACPEVRNT 126
 QY 116 ----- 115
 Db 127 PWTPLPVNVTGGARQERFRTCTRAPLPDPHGLQFGKRTETRTCTPADGTGACDADAL 186
 QY 116 -----VHGAWSAWOPWGTCSBSCGKGTQTRARLNNPPAPFGSYCDGAET 161
 Db 187 VEDLLRSGSTSPHTLNGGWATWGPWSSCSRDCBLGFRVRKRTCTNPEPRNGGLPCVGDAA 246
 QY 162 QMVCNERNCPHGWATWASWASACSVSCGGARQRTGCSDPV 206
 Db 247 EYQDCNPAQCPVRGAWSCWTAWSCSASCGGHHYQRTSCTSPAP 291

RESULT 11

Q6ZPQ8 PRELIMINARY; PRT; 632 AA.
 ID Q6ZPQ8
 AC Q6ZPQ8
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE MKTAA1445 protein (Fragment).
 GN Name=MKTAA1445;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic tail;
 RX PubMed=14621295;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
 RA Saga Y., Nagase T., Ohara O., Koga H.;
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
 RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries.";
 RL DNA Res. 10:167-180(2003).
 DR EMBL; AK129362; BAC98172.1; -;
 DR EMBL; AK129362; BAC98172.1; -;
 FT NON TER
 SQ SEQUENCE 632 AA; 69037 MW; 78CD7F28C3FF3E7 CRC64;
 Query Match 41.2%; Score 507.5; DB 2; Length 632;
 Best Local Similarity 31.9%; Pred. No. 2e-32;
 Matches 91; Conservative 26; Mismatches 81; Indels 87; Gaps 3;
 QY 3 HGGFSONAWRACSVTCGKIQKSRCLNCPPLPANGKPCQGSLEMRNC-QNKPCPDVG 61
 Db 145 NGAWTANSSWAQCTSCGIGFQVRQSCSNPAPRHGGRICVGRSRERFCNENTPCFVPI 204
 QY 62 SWEWSLWEECTRCGRGNQTRTCTNNPSVQHGGRPCGNAVEIIMCNRPCP----- 115
 Db 205 FWASWGSWSKSCNNCGGVQSRSSCEN-----GNSCPGCGVEFKTCNPEACPEVRNT 258
 QY 116 ----- 115
 Db 259 PWTPLPVNVTGGARQERFRTCTRAPLPDPHGLQFGKRTETRTCTPADGTGACDADAL 318
 QY 116 -----VHGAWSAWOPWGTCSBSCGKGTQTRARLNNPPAPFGSYCDGAET 161
 Db 319 VEDLLRSGSTSPHTLNGGWATWGPWSSCSRDCBLGFRVRKRTCTNPEPRNGGLPCVGDAA 378

RESULT 12

BAC98172 PRELIMINARY; PRT; 632 AA.
 ID BAC98172
 AC BAC98172
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE MKTAA1445 protein (Fragment).
 GN Name=MKTAA1445;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic tail;
 RX PubMed=14621295;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
 RA Saga Y., Nagase T., Ohara O., Koga H.;
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
 RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries.";
 RL DNA Res. 10:167-180(2003).
 DR EMBL; AK129362; BAC98172.1; -;
 DR EMBL; AK129362; BAC98172.1; -;
 FT NON TER
 SQ SEQUENCE 632 AA; 69037 MW; 78CD7F28C3FF3E7 CRC64;
 Query Match 41.2%; Score 507.5; DB 2; Length 632;
 Best Local Similarity 31.9%; Pred. No. 2e-32;
 Matches 91; Conservative 26; Mismatches 81; Indels 87; Gaps 3;
 QY 3 HGGFSONAWRACSVTCGKIQKSRCLNCPPLPANGKPCQGSLEMRNC-QNKPCPDVG 61
 Db 145 NGAWTANSSWAQCTSCGIGFQVRQSCSNPAPRHGGRICVGRSRERFCNENTPCFVPI 204
 QY 62 SWEWSLWEECTRCGRGNQTRTCTNNPSVQHGGRPCGNAVEIIMCNRPCP----- 115
 Db 205 FWASWGSWSKSCNNCGGVQSRSSCEN-----GNSCPGCGVEFKTCNPEACPEVRNT 258
 QY 116 ----- 115
 Db 259 PWTPLPVNVTGGARQERFRTCTRAPLPDPHGLQFGKRTETRTCTPADGTGACDADAL 318
 QY 116 -----VHGAWSAWOPWGTCSBSCGKGTQTRARLNNPPAPFGSYCDGAET 161
 Db 319 VEDLLRSGSTSPHTLNGGWATWGPWSSCSRDCBLGFRVRKRTCTNPEPRNGGLPCVGDAA 378

RESULT 13

SM5B MOUSE
 ID SM5B MOUSE
 AC SM5B MOUSE
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Semaphorin 5B precursor (Semaphorin G) (Sema G).
 GN Name=Sema5b; Synonyms=SEMA5, SemG;
 OS Mus musculus (Mouse).
 QY 162 QMVCNERNCPHGWATWASWASACSVSCGGARQRTGCSDPV 206
 Db 379 EYQDCNPAQCPVRGAWSCWTAWSCSASCGGHHYQRTSCTSPAP 423

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI;
 RX MEDLINE=96414430; PubMed=8817451;
 RA Adams R.H., Betz H., Puechel A.W.;
 RT "A novel class of murine semaphorins with homology to thrombospondin
 is differentially expressed during early embryogenesis.";
 RL Mech. Dev. 57:33-45(1996).
 CC -!- FUNCTION: May act as positive axonal guidance cues.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: In adult, only detected in brain.
 CC -!- DEVELOPMENTAL STAGE: Differentially expressed in embryonic and
 adult tissues. Its abundance decreases from E10 to birth.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 7 TSP type-1 domains.
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 or send an email to license@isb-sib.ch).

 DR EMBL; X97818; CA466398.1; -;
 DR HSSP; P07996; ILSL.
 DR MGD; MGI:107555; Sema5b.
 DR InterPro; IPR0031659; Sema5b.
 DR InterPro; IPR002165; plexin-like.
 DR InterPro; IPR001627; Sema.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR Pfam; PF00090; TSP 1; 5.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00423; PSI; 1
 DR SMART; SM00630; Sema; 1.
 DR SMART; SM00209; TSP1; 5.
 DR PROSITE; PS1004; Sema; 1.
 DR PROSITE; PS50092; TSP1; 5.
 DR PROSITE; PS50092; TSP1; 5.
 KW Developmental protein; Glycoprotein; Multigene family; Neurogenesis;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 1093 Semaphorin 5B.
 FT DOMAIN 20 978 Extracellular (Potential).
 FT TRANSMEM 979 999 Potential.
 FT DOMAIN 1000 1093 Cytoplasmic (Potential).
 FT DOMAIN 45 495 Sema.
 FT DOMAIN 551 605 TSP type-1 1.
 FT DOMAIN 606 662 TSP type-1 2.
 FT DOMAIN 664 713 TSP type-1 3.
 FT DOMAIN 721 776 TSP type-1 4.
 FT DOMAIN 795 850 TSP type-1 5.
 FT DOMAIN 852 907 TSP type-1 6.
 FT DOMAIN 908 952 TSP type-1 7.
 FT CARBOHYD 59 59 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 157 157 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 287 287 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 333 333 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 378 378 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 532 532 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 539 539 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 547 547 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 602 602 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 728 728 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 944 944 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 1093 AA; 120326 MW; 295C9B1E8108717 CRC64;
 Query Match 41.2%; Score 507.5; DB 1; Length 1093;
 Best Local Similarity 31.9%; Pred. No. 3.3e-32;
 Matches 91; Conservative 26; Mismatches 81; Indels 87; Gaps 3;
 QY 3 HGFSSWSAWRACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDDLEMRNC-QNKPCPVDG 61
 Db 606 NGAWTANSSWAQSTSCGIGFVQRSCSNPAPRHGGRICVGRSRERFCNENTPCVPPI 665
 QY 62 SWSWSLWEECTSCGRGNQTRTRTCNNPVSQVHGGRPCGNAVEIIMCNRPCP----- 115
 Db 666 FWASGWSKCSNNCGGVQSRRCSEN-----GNSCPGCGVEFTCNPEACPEVRNT 719
 QY 116 ----- 115
 Db 720 PWTPLPVNTVQGARQQRPRFTCRAPLPDPHGLQFKERTETRTCPADGTACD DAL 779
 QY 116 -----VHGASWAFQWGTCSGKGTOTRLCNPPPPFGGSGYCDGAET 161
 Db 780 VEDLLRSGSTSPHPLNGWATGWSSCSRDCELGPRVKRTCTNPEPRNGGLPCVGDAA 839
 QY 162 QMVCNERNCPHGWATWASWACSVCSCGGARQRTGSDPVP 206
 Db 840 EYQDNCFPACPVGAWSCWTAWSCQSCGCGHYQRTSCTSPAP 884

 RESULT 14
 QSPCK8 PRELIMINARY; PRT; 1088 AA.
 AC Q6PCK8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MG068835 protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
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 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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 RN [2]
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 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 initiative.";
 Dev. Dyn. 225:384-391 (2002).
 RL

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RN RA KLAUSNER R.D., COLLINS F.S., WAGNER L., SHENMEN C.M., SCHULER G.D.,
RC ALTSCHUL S.F., ZEEBERG B., BUETOW K.H., SCHAEFER C.F., BHAT N.K.,
RC HOPKINS R.F., JORDAN H., MOORE T., MAX S.I., WANG J., HSIEH F.,
RA DIACHENKO L., MARUSINA K., FARMER A.A., RUBIN G.M., HONG L.,
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RA BROWNSTEIN M.J., USUDIN T.B., TOSHIYUKI S., CARNINCI P., PRANGE C.,
RA RAHA S.S., LOQUELLANO N.A., PETERS G.J., ABRAMSON R.D., MULLAHY S.J.,
RA BOSAK S.A., MCEWAN P.J., MCKERNAN K.J., MALEK J.A., GUNARATNE P.H.,
RA RICHARDS S., WORLEY K.C., HALE S., GARCIA A.M., GAY L.J., HULYK S.W.,
RA VILLALON D.K., MUZYNI D.M., SODERGREN E.J., LU X., GIBBS R.A.,
RA FAHEY J., HELTON E., KETTEMAN M., MADAN A.C., RODRIGUES S., SANCHEZ A.,
RA WHITING M., MADAN A., YOUNG A.C., SHEVCHENKO Y., BOUFFARD G.G.,
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RT "Generation and initial analysis of more than 15,000 full-length human
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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RA Klein S., Strausberg R.;
RL EMBL: BC059288; AAH59288.1; -
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR InterPro: IPR003659; Pfam-like.
DR InterPro: IPR002165; Pfam-like.
DR InterPro: IPR001627; Pfam.
DR InterPro: IPR000884; TSP1.
DR InterPro: IPR000885; TSP1.
DR Pfam: PF01437; PSI; 1.
DR Pfam: PF00900; TSP1; 5.
DR PRINTS: PR01705; TSP1REFAT.
DR SMART: SM00423; PSI; 1.
DR SMART: SM00630; TSP1; 1.
DR SMART: SM00209; TSP1; 6.
DR PROSITE: PS0092; TSP1; 6.
SQ SEQUENCE 1088 AA; 122657 MW; 4DFCD371A7CD8176 CRC64;

Query Match 41.1%; Score 506.5; DB 2; Length 1088;
Best Local Similarity 31.2%; Pred. No. 3.9e-32;
Matches 89; Conservative 31; Mismatches 78; Indels 87; Gaps 3;

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Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 662 FWTSGSWTKCSDCGGTHSRQSCEN-----GNTCPGCTMEFRTCNPEPCPEVRNT 715
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 ----- 115
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QY 116 -----VHGAWSAWOPWGTCSGKGTQTRARLCNNPPAPFGGSGYCDGAET 161
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 776 VDDLNRNSKTSGLIINGWSLWSWSSCSRDCQGFPRSRKRTCSNPEPRKGLPCTGSAM 835
QY 162 QMOVCNERNCPIHGKWATWASWSACSVCGGGARQRTGCSDPVP 206
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DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68835 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
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CX NCBI_TaxID=8355;
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RT initiative.";
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RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA KLAUSNER R.D., COLLINS F.S., WAGNER L., SHENMEN C.M., SCHULER G.D.,
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RA KRZYWINSKI M.I., SKALSKA U., SMALIUS D.E., SCHNERCH A., SCHEIN J.E.,
RA JONES S.J., MARRA M.A.;
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QY 836 EYQDCNPQPCFVKGSWCSWSPWTCQCATCGGHHYQRTCTCTNPPP 880
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